PATENT

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for

METHODS AND COMPOSITIONS RELATING TO A CARDIAC-SPECIFIC NUCLEAR REGULATORY FACTOR

by

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BACKGROUND OF THE INVENTION

The government owns rights in the application pursuant to NIH Grant Nos. P01 HL49953 and HL63926.

1. Field of the Invention

The present invention relates generally to the fields of developmental biology and molecular biology. More particularly, it concerns proteins involved in the regulation of cardiomyocyte cell growth and development.

2. Description of Related Art

The leading cause of morbidity and mortality in industrialized countries is heart disease, particularly heart disease that is associated with myocardial infarction. Myocardial infarction results in the loss of cardiomyocytes. Cardiomyocytes are post-mitotic cells and generally do not regenerate after birth. Furthermore, it has been discovered that they respond to mitotic signals by cell hypertrophy (Kodama *et al.*, 1997; Pan *et al.*, 1997) rather than by cell hyperplasia. The loss of cardiomyocytes leads to regional contractile dysfunction. In addition, the necrotized cardiomyocytes in the infarcted regions in the ventricular tissues are progressively replaced by fibroblasts to form scar tissue.

Recently, fetal cardiomyocytes transplanted in heart scar tissue limited scar expansion and prevented postinfarction heart failure (Leor *et al.*, 1996). Although the transplantation of fetal cardiomyocytes is a proposed treatment of heart failure, it remains impractical in the clinical setting, in part because of the difficulty of obtaining fetal heart donor tissue. Thus, it is desirable to develop a cardiomyogenic cell line that could be used to facilitate the understanding of cardiomyocyte development and to facilitate the treatment of heart diseases, such as those associated with loss of cardiomyocytes.

Although it is known that the loss of post-mitotic cardiomyocytes results in increased morbidity and mortality, very little is known about the genes that are involved

in heart development. It is known that transcription factors such as d-HAND, e-HAND (Srivastava *et al.,* 1995), MEF-2C (Edmondson *et al.* 1994; Lin *et al.* 1997), Nkx2.5/Csx, GATA4, and TEF-1 play important roles in cardiac development (Harvey, 1996), but the lack of a model for cardiomyocyte differentiation has hindered the understanding of the interactions of these genes.

A recent report revealed that murine marrow stromal cells that are treated with 5-azacyidine, a cytosine analog capable of altering expression of certain genes that may regulate differentiation, results in a cell line that differentiates into cardiomyocytes *in vitro* (Makino *et al.*, 1999). This cardiomyogenic cell line demonstrated several phenotypic characteristics that are specific to cardiomyocytes, *e.g.,* adjoining cells via intercalated discs, forming myotubes, and beating spontaneously. In addition, the expression of cardiomyocyte specific genes, such as homeobox gene Nkx2.5, alpha-myosin heavy chain and atrial natriuretic factor, also are considered characteristic.

Although the proposed transplantation of fetal cardiomyocytes and cardiomyogenic cell lines are possible treatments, it is preferable to discover a treatment that eliminates any donor/species problems. Thus, identifying new regulators of cardiomyocyte growth and differentiation is an important goal in the search for therapeutics to treat myocardial tissue damage.

SUMMARY OF THE INVENTION

The present invention provides polypeptides capable of modulating cell phenotype, particularly phenotypic characteristics of cardiomyocyte cells, and polynucleotides encoding such polypeptides. In particular, provided herein is a family of peptides, known as myocardins, that share certain sequence homology and functional activities, as described herein. In one aspect, the polypeptides of the present invention comprise mycardin peptides and biologically active fragments thereof. In another aspect, the present invention provides isolated polynucleotides encoding a myocardin peptide including fragments thereof. Exemplary biologically active fragments of myocardin polypeptides are also provided herein.

In a further aspect, there are provided expression cassettes comprising polynucleotides encoding the polypeptides of the present invention. Preferably, such expression cassettes further comprise one or more regulatory sequences operably linked to said polynucleotide, capable of enhancing or otherwise modulating transcription and/or translation of said polynucleotide in a target cell, for example a mammalian cell. By way of illustration, in one embodiment, an expression cassette comprising a polynucleotide encoding a myocardin polypeptide operably linked to a promoter is provided. The promoter may be an inducible promoter or a constitutive promoter. The promoter may be heterologous to the myocardin coding sequence. Further, the promoter may be a ubiquitous promoter, for example a cytomeglovirus (CMV) promoter, rous sarcoma virus (RSV) promoter or human elongation factor (*e.g.*, hEF-1α) promoter, or it may be active only in certain tissues/cells for example a fibroblast specific promoter (*e.g.*, an alpha collagen promoters) or a muscle-specific promoter (*e.g.*, a myosin light chain-2 promoter or a α-myosin heavy chain). The regulatory sequence of the expression cassette may further comprise a polyadenylation signal. The expression cassette may be a viral expression construct, for example, a retroviral vector, an adenoviral vector, an adeno-associated viral vector, a vaccina viral vector, a herpesviral vector, a polyoma viral construct, lentiviral vector or a Sindbis viral vector. The expression cassette may further comprise a second polynucleotide encoding a second polypeptide. The second polypeptide may be, for example, a cardiac transcription factor.

In another aspect of the present invention, there is provided an isolated nucleic acid segment comprising at least 15 contiguous nucleotides of SEQ ID NO: 1, SEQ ID NO: 25, SEQ ID NO: 27 or SEQ ID NO: 29. Also provided is an isolated nucleic acid segment of SEQ ID NO: 1, SEQ ID NO: 25, SEQ ID NO: 27 or SEQ ID NO: 29 comprising 15-2000 nucleotides in length. In a related aspect, there is provided a peptide of 8-50 residues comprising at least 8-12 consecutive residues of SEQ ID NO: 2, SEQ ID NO: 26, SEQ ID NO: 28 or SEQ ID NO: 30. In another related aspect, there are provided antibodies, which may be produced by a hybridoma cell, that bind immunologically to a polypeptide comprising SEQ ID NO: 2, SEQ ID NO: 26, SEQ ID NO: 28 or SEQ ID NO: 30, or an antigenic fragment thereof. The antibodies may be monoclonal or polyclonal antisera.

In a further aspect of the present invention, as described further below, myocardin peptides from different species are provided. By way of illustration, murine mycardin 1 (*e.g.*, SEQ ID NOS: 2 and 30), human myocardin 1 (*e.g.*, SEQ ID NOS: 26 and 28), human myocardin 2 (SEQ ID NO: 4) and human myocardin 3 (SEQ ID NO: 6) are described. These myocardin peptides share localized regions of high amino acid sequence homology, particularly in the carboxyl-terminal transcription activation domain, and, particularly with respect to myocardin 1 and 2, in glutamine (Q) rich domains.

In still a further aspect of the invention, there is provided a transformed host cell comprising a polynucleotide encoding a myocardin polypeptide and a promoter heterologous to the myocardin-encoding polynucleotide which promoter directs the expression of the myocardin polypeptide. The host cell may be prokaryotic or eukaryotic. In a related aspect of the invention, there is provided a method of using the transformed host cell and culturing it under conditions suitable for the expression of the myocardin polypeptide. In yet another aspect, there is provided a fusion protein comprising a myocardin protein or peptide fused to a second protein or peptide.

As discussed above, heart disease, especially that resulting in a heart attack, typically results in significant cardiac dysfunction. This dysfunction can be the result of the activities of cells, especially non-cardiomyocyte cells, in the region of disease of the heart. In a further aspect of the present invention, compositions and methods are provided that alleviate the deleterious activities of such non-cardiomyocyte target cells on the functioning of the heart by modulating the phenotype of said target cells. In preferred embodiments, the compositions and methods not only alleviate the deleterious activities of the target cell population but stimulate the target cells to engage in one or more functions typical of cardiomyocytes thereby improving myocardial functioning in the diseased region. By way of illustration, fibroblast cells typically are recruited to form scar tissue in areas of myocardium where cardiomyocyte necrosis has occurred (for example, as the result of myocardial infarction) thereby resulting in permanent, regional cardiac dysfunction. Introduction of a composition in accordance herewith into such fibroblasts can prevent those cells from engaging in such deleterious activity and, in preferred embodiments, can actually stimulate the fibroblasts to engage in one or more

functions phenotypical of cardiomyocytes (for example, spontaneous beating, formation of microtubules or adjoining to neighboring cells via intercalated discs, and expression of cardiomyocyte specific genes, such as homeobox gene Nkx2.5, alpha-myosin heavy chain and atrial natriuretic factor) thereby assisting heart function. Advantageously, introduction of such compositions in accordance herewith may additionally improve the functioning of existing cardiomyocytes by, for example, inducing hypertrophy therein. Thus, the present compositions may serve the dual roles of stimulating fibroblast cells to engage in function(s) phenotypic of cardiomyocytes and stimulating hypertrophy in existing cardiomyocytes.

In yet a further and related aspect of the present invention, there is provided a method of converting a non-cardiomyocyte target cell, such as a cardiac fibroblast into a cardiac myocyte-like cell comprising introducing into the target cell an expression cassette. The expression cassette comprises a polynucleotide encoding a myocardin polypeptide as well as one or more regulatory sequences, for example, a promoter with or without enhancer sequences, which regulatory sequences are active in the target cell and direct the expression of the polypeptide. The method may further comprise measuring cardiac and muscle cell lineage markers. In another aspect, the expression cassette may further comprise one or more additional polynucleotides encoding one or more polypeptides. By way of illustration, a second polypeptide may be a cardiac transcription factor, for example, GATA4. In a related aspect, expression of the additional polynucleotides may be under the control of the same regulatory sequences as the first polynucleotide or may be separately controlled by additional regulatory sequences.

In another aspect of the present invention, the method further comprises introducing one or more additional expression cassettes into target cells separately from introduction of the myocardin expression cassette. By way of illustration, a second expression cassette comprising a polynucleotide encoding a second polypeptide and including a second promoter able to direct expression of the second polypeptide in the target cells may be delivered to the target cell using a separate gene delivering means from that used to introduce the myocardin expression cassette. Thus, for example, a first gene delivery vector comprising a myocardin expression cassette may be delivered

simultaneously or contemporaneously with a second gene delivery vector comprising a second expression cassette. If desired, polypeptide expression may be measured, for example, by measuring transcription by RNA hybridization, RT-PCR or Western analysis.

In yet another aspect, there is provided a method of generating a cardiomyocyte comprising introducing into a cardiac fibroblast an expression cassette. The expression cassette comprising, for example, a polynucleotide encoding a myocardin polypeptide operatively linked to a promoter capable of directing expression of the polypeptide. The promoter may be heterologous to the coding sequence and may be a ubiquitous (*e.g.*, CMV) or a specific promoter (*e.g.*, an alpha collagen promoter). The expression cassette may be introduced into the fibroblast by any of a variety of means known to those of skill in the art. By way of illustration, lipid-based vectors (*e.g.*, liposomes), viral vectors (*e.g.*, retroviral vectors, vaccina viral vectors, herpesviral vectors, polyoma viral constructs, lentiviral vectors or Sindbis viral vectors), or other macromolecular complexes capable of mediating delivery of the polynucleotide to the fibroblast or other target cell, may be employed. In a further aspect the gene delivery vector may be modified, for example by means known to those of skill in the art, to target one or more specific cell types. The expression cassette may also comprise a selectable marker, *e.g.*, an immunologic marker. The expression cassette may further comprise a second polynucleotide encoding a second polypeptide, such as the GATA4 cardiac transcription factor. Such a second polynucleotide may be under control of a second promoter or the same promoter as the first polynucleotide. Alternatively, an internal ribosomal entry site (IRES) may be employed between the two transgenes to permit expression of the second transgene.

In a further aspect of the present invention, there is provided a method of stimulating cardiac tissue regeneration comprising inhibiting the function of myocardin in a post-mitotic cardiomyocyte. Inhibiting may comprise providing antisense nucleic acid that inhibits transcription or translation of a myocardin mRNA. The antisense nucleic acid may be provided by introducing an expression cassette encoding myocardin antisense RNA.

In still another aspect, there is provided a non-human transgenic animal, *e.g.*, a mouse, comprising an expression cassette. The expression cassette comprises a polynucleotide encoding a myocardin peptide or protein and a promoter operably linked thereto which promoter may be heterologous to the myocardin peptide or protein encoding region. The promoter may be a constitutive or an inducible promoter. The expression cassette may further comprise selectable marker(s). In a related aspect of the present invention, the non-human transgenic animal may comprise a defective germ-line myocardin allele or two defective germ-line myocardin alleles.

In a further aspect of the invention, there is provided a method of treating a heart disease, such as cardiomyopathy (for example, myocardial infarction or hypertension). The method comprises administering to an animal suffering from a heart disease an expression cassette, which may comprise a polynucleotide encoding a myocardin peptide or protein and a promoter operable in eukaryotic cells. The promoter may be a tissue-specific promoter. The expression cassette may be comprised within a viral expression vector, for example, a retroviral vector, an adenoviral vector, an adeno-associated viral vector, a vaccina viral vector, a herpesviral vector, a polyoma viral construct, a lentiviral vector or a Sindbis viral vector or within a non-viral vector, for example a lipid-based vector. In a related aspect, the method may comprise providing to an animal suffering therefrom a myocardin antisense nucleic acid.

In another related aspect, there is provided a method of alleviating one or more symptoms of a heart disease comprising inhibiting the function of myocardin in post-mitotic cardiomyocytes in the subject. Another method of alleviating one or more symptoms of a heart disease, for example in a subject with heart failure, comprises increasing the level of myocardin in fibroblasts to generate cardiomyocytes in the subject.

An additional aspect of the present invention is to provide compositions and methods for the identification of downstream target genes of myocardin polypeptides. A gene delivery vector, for example an adenoviral vector, can be employed to deliver a myocardin gene to isolated cardiomyocytes thereby permitting over-expression of the myocardin polypeptide. Differences in gene profiling between control (*i.e.*, non-

transfected) cardiomyocytes and transfected (*i.e.*, myocardin-overexpressing) cardiomyocytes can then be assessed by standard methods, such as differential display and microarray (*e.g.*, gene chip) technology. Genes that are activated by myocardin in cardiomyocytes can subsequently be evaluated as potential therapeutics, for example, using bioinformatics techniques. In yet another aspect of the present invention, there is provided a method of screening for a candidate substance for an effect on myocardin regulation of cardiomyocyte development comprising: (a) providing myocardin and GATA to a cell; (b) admixing myocardin and GATA in the presence of the candidate substance; and (c) measuring the effect of the candidate substance on the expression of a cardiac lineage marker, wherein a difference in the expression of the cardiac lineage marker, as compared to an untreated cell, indicates that the candidate substance effects myocardin regulation of cardiomyocyte development.

Exemplary cells include fibroblast and cardiomyocytes, which may be located in an animal. The modulator may increase or decrease the expression of the cardiac lineage marker. The cardiac lineage marker may be Nkx2.5. The measuring of the expression of the cardiac lineage marker may comprise RNA hybridization, RT-PCR, immunologic detection, ELISA or immunohisotchemistry, for example.

In still yet another aspect of the invention, there is provided a method of screening for a modulator of myocardin expression comprising: (a) providing a cell that expresses a myocardin polypeptide; (b) contacting the myocardin polypeptide with a candidate substance; and (c) measuring the expression of myocardin, wherein a difference in myocardin expression, indicates that the candidate substance is a modulator of myocardin expression. The modulator may be a pharmaceutical composition. The modulator may enhance or inhibit myocardin expression.

In another aspect of the invention, there is provided a method of screening a candidate substance for myocardin binding activity comprising: (a) providing a myocardin polypeptide; (b) contacting the myocardin polypeptide with the candidate substance; and (c) determining the binding of the candidate substance to the myocardin

polypeptide. The assay may be performed in a cell free system, a cell or *in vivo*. The candidate substance may be an inhibitor or an enhancer of myocardin.

BRIEF DESCRIPTION OF THE DRAWINGS

The following drawings form part of the present specification and are included to further demonstrate certain aspects of the present invention. The invention may be better understood by reference to one or more of these drawings in combination with the detailed description of specific embodiments presented herein.

FIG. 1 Schematic diagram of the events of cardiac development. Cardiac precursors from the cardiac crescent (left) migrate to the midline of the embryo to form the linear heart tube, which undergoes rightward looping and eventual formation of the mature four-chambered heart. Different populations of cardiac precursor cells fated to form the aortic sac (AS), conotruncus (CT), right ventricle (RV), left ventricle (LV), and atria (A) are shown. A schematic diagram of the structure of the mouse myocardin 1 gene is also shown. Based on human genomic sequence in public databases, we have determined that the human gene maps to chromosome 17 and encompasses 170 kb.

FIG. 2 Amino acid and nucleotide sequence of N-terminally truncated myocardin 1. A nucleotide sequence encoding an N-terminally truncated myocardin 1 and the corresponding amino acid sequence are shown.

FIG. 3A-C Expression pattern of myocardin 1 during early heart development. FIG. 3A: Expression of myocardin 1was determined by whole-mount to mouse embryos at E7.75. Myocardin 1 transcripts can be seen localized to the cardiac crescent. FIG. 3B: Expression of myocardin 1 was determined by section to mouse embryos at E8.0. Transcripts are present throughout the heart tube in a transverse section. FIG. 3C: Expression of myocardin 1 was determined by *in situ* hybridizations to mouse embryos at E12.5. Transcripts are seen throughout the developing heart in a sagittal section.

FIG. 4 Expression pattern of myocardin 1 in adult mouse tissues. The expression of myocardin 1 transcripts in adult mouse tissues was analyzed by Northern blot. Transcripts are detected only in the heart. Size markers are shown to the left.

FIG. 5 Nuclear localization of myocardin 1 protein. Cos cells were transiently transfected with an expression vector encoding myocardin 1 with a Flag-epitope tag. The subcellular location of myocardin 1 protein was determined by immunostaining with anti-Flag antibody. The myocardin 1 protein is substantially localized to the nucleus. The inset in the lower right corner shows an enlargement of a single cell, with strong myocardin 1 staining in the nucleus, but excluded from the nucleoli.

FIG. 6 Structure of myocardin 1 and mapping of transcription activation domains. A schematic diagram of myocardin 1 is shown at the top. The nuclear localization sequence (NLS) is located between residues 117 and 126, within a basic region. A glutamine-rich (Q) domain is located between residues 159-192. The transcription activation domain is located at the carboxyl-terminus. Portions of myocardin 1 were fused to the DNA binding domain of yeast GAL4 and tested in transfected Cos cells for transcriptional activity against a GAL4-dependent luciferase reporter. Relative transcriptional activities of different myocardin 1 fragments are shown at the bottom. The carboxyl-terminus is an extremely potent transcription activation domain, able to activate the reporter over 1000-fold, to a level comparable to that of the powerful viral coactivator VP16 (not shown).

FIG. 7A-D Trans-activation of the *SM22* promoter by myocardin 1. Cos cells were transiently transfected with a luciferase reporter gene containing the 1.4 kb SM22 promoter and expression vectors encoding myocardin 1 and SRF, as indicated. Forty eight hr later, cells were harvested and luciferase activity was assayed. FIG. 7A: shows activity of the wild-type *SM22* promoter, which is transactivated about 100-fold by myocardin 1. FIG. 7B: shows activity of the *SM22* promoter with a mutation in the distal CArG box (CArG-far). This promoter is also activated by myocardin 1, but not to the same extent as the wild-type promoter. FIG. 7C: shows activity of the *SM22* promoter with a mutation in the proximal CArG box (CArG-near). This promoter has lost almost all responsiveness to myocardin 1, as has the promoter with both CArG boxes mutated (FIG. 7D).

FIG. 8 Myocardin 1 and MEF2C cooperatively activate the MLC2V promoter. Cos cells were transiently transfected with a luciferase reporter gene containing the MLC2V promoter and expression vectors encoding myocardin 1 and MEF2C, as indicated. Forty eight hours later, cells were harvested and luciferase activity was assayed. The results show that myocardin 1 and MEF2C synergistically activate MLC2V transcription.

FIG. 9 GATA4 represses myocardin 1 activation of the ANF promoter. HeLa cells and Cos cells were transiently transfected with a luciferase reporter gene containing the ANF promoter and expression vectors encoding myocardin 1 and GATA4 (1 = 100 ng anf-luc; 2 = 100 μg anf-luc, 100 ng myocardin; 3 = 100 ng anf-luc, 10 ng GATA4; 4 = 100 ng anf-luc, 20 ng GATA4; 5 = 100 ng anf-luc, 50 ng GATA4; 6 = 100 ng anf-luc, 100 ng GATA4; 7 = 100 ng anf-luc, 100 ng myocardin, 10 ng GATA4; 8 = 100 ng anf-luc, 100 ng myocardin, 20 ng GATA4; 9 = 100 ng anf-luc, 100 ng myocardin, 50 ng GATA4; 10 = 100 ng anf-luc, 100 ng myocardin, 100 ng GATA4). Forty eight hours later, cells were harvested and luciferase activity was assayed. The results show that activation of ANF transcription by myocardin 1 is repressed in the presence of GATA4.

FIG. 10 Myocardin 1 and Nkx2.5 cooperatively activate the α-MHC promoter. HeLa cells were transiently transfected with a luciferase reporter gene containing the α-MHC promoter and expression vectors encoding myocardin 1 and Nkx2.5, as indicated. Forty eight hr later, cells were harvested and luciferase activity was assayed. The results show that myocardin 1 and Nkx2.5 synergistically activate α-MHC transcription.

FIG. 11 Overexpression of myocardin induces serial assembly of sarcomeres in cardiomyocytes. Cardiomyocytes were infected with adenoviruses expressing either myocardin(Ad-myocardin) or ß-galactosidase(Ad-LacZ), serum deprived, and immunostained with anti-sarcomeric-α-actininat antibody 24 hour post-infection.

FIG. 12 Overexpression of myocardin induces ANF expression in cardiomyocytes. Cardiomyocytes were infected with adenoviruses expressing either myocardin (Ad-myocardin) or ß-galactosidase (Ad-LacZ), serum deprived, and

immunostained with anti-ANF antibody 24 hour post-infection. Images were captured at two different magnifications (x20, x100).

FIG. 13 GATA4 and myocardin 1 activate of the NKX2.5 promoter. HeLa cells and Cos cells were transiently transfected with a luciferase reporter gene containing the NKX2.5 promoter and expression vectors encoding myocardin 1 and GATA4 (1 = 100 ng nkx-luc; 2 = 100 ng nkxf-luc, 500 ng myocardin; 3 = 100 ng nkx-luc, 10 ng GATA4; 4 = 100 ng nkx-luc, 20 ng GATA4; 5 = 100 ng nkx-luc, 50 ng GATA4; 6 = 100 ng nkx-luc, 100 ng GATA4; 7 = 100 ng nkx-luc, 500 ng myocardin, 10 ng GATA4; 8 = 100 ng nkx-luc, 500 ng myocardin, 20 ng GATA4; 9 = 100 ng nkx-luc, 500 ng myocardin, 50 ng GATA4; 10 = 100 ng nkx-luc, 500 ng myocardin, 100 ng GATA4). Forty eight hours later, cells were harvested and luciferase activity was assayed. The results show activation of NKX2.5 transcription by myocardin 1 and GATA4.

DESCRIPTION OF ILLUSTRATIVE EMBODIMENTS

Heart disease is the number one cause of death and hospitalization in the industrialized world, due in large part to the irreversible nature of the damage sustained by the heart following heart attack and other acquired and congenital diseases. At present, the only means of repairing a damaged heart is through complicated surgery and/or heart transplant, which have obvious financial and medical shortcomings for the patient. The possibility of regenerating cardiac muscle cells within the intact human heart following damage represents one of the most important challenges in cardiovascular medicine. Perhaps the greatest chance for success in this area is to identify "master" control genes for cardiac development and to use these genes to reprogram non-muscle cells to a cardiac muscle cell fate.

A major barrier to cardiac regeneration is the inability of postnatal cardiomyocytes to divide. In principle, cardiac repair could be achieved through a release from this block to cell cycle progression. However, such an approach, which might involve introduction of oncogenes or other powerful stimulators of cell proliferation into the heart, has an obvious downside unless such regulators were

somehow cardiac-specific and could be prevented from inducing uncontrolled proliferation of other cell types. Because about 40% of the cells in the myocardium are fibroblasts, an alternate approach would be to reprogram these cells to a cardiomyocyte fate at sites of cardiac damage through targeted delivery of cardiac master control genes.

The loss of cardiomyocytes leads to reduced contractile function of the heart resulting in increased morbidity and mortality. The present inventors now report the discovery of novel cardiac-specific factors, referred to herein as myocardins. One such myocardin, myocardin 1, is expressed in cardiac and smooth muscle. Moreover, myocardin 1 is first expressed as early as the linear heart tube stage, embryonic day 8 (E8) in the mouse. This expression is restricted to the heart and to a subset of vascular smooth muscle cells throughout embryogenesis to adulthood. The subcellular distribution of myocardin 1 is localized in the nucleus. Moreover, expression of myocardin 1 in transfected cells appears to result in growth arrest of the cells.

To determine the functions of myocardin 1, the inventors transfected myocardin 1 expression plasmids into fibroblasts (Cos and HeLa cells) along with expression plasmids for the cardiac transcription factor GATA4. The cells were transiently transfected using FuGENE 6 (Boehringer-Mannheim), according to manufacturer's instructions. Briefly, 0.1 μg of expression plasmid encoding myocardin 1 or the other indicated cardiac transcription factors, along with the indicated luciferase plasmids, were mixed with 3 μl of FuGENE 6 and added to cells in six-well plates. Cells were harvested 48 hr later and luciferase activity was determined in cell extracts. In all transfections, the amount of DNA per well was kept constant by adding the corresponding vector. CMV-lacZ, which contains the lacZ gene under control of the constitutive cytomegalovirus promoter, was included in all transfections as an internal control to normalize for variations in transfection efficiency. The results demonstrated that myocardin 1, plus GATA4, transactivates regulatory sequences for the cardiac specific homeobox Nkx2.5, which is the earliest marker for the cardiac lineage in vertebrates. These results indicate that myocardin 1 plays an important role in regulating cardiomyocyte development.

Based upon the functional activity of the murine myocardin 1 and having its complete cDNA sequence, the inventors have been able to identify other myocardins, which they have characterized. Initial searches of DNA sequence databases with myocardin 1 sequence revealed a number of related sequences. Most of these sequences are short sequences (for example, ESTs) that share homology to only small regions of myocardin 1. None of the sequences located have been identified as encoding proteins having any particular function, much less any fuction related to cell regulation, particularly cardiac cell regulation. However, using these techniques in combination with the information obtained previously regarding the murine myocardin, the inventors have identified two sequences that share significant homology with myocardin 1. These appear to be partial sequences from two additional myocardin genes. cDNA clones for these two related genes, now designated myocardin 2 and myocardin 3, have been obtained. A comparison of the three myocardin species identified has revealed localized regions of high amino acid homology between the proteins, particularly in the carboxyl-terminal transcription activation domain. By Northern analysis, it was shown that that myocardin 2 is ubiquitous, and that myocardin 3 appears restricted to heart and liver. These factors may be dimerization partners for myocardin 1, and/or may serve analogous functions to myocardin 1 in the heart and/or other tissues.

Using similar techniques and information about the murine myocardin 1, the inventors have also been able locate the genomic sequence of the human homolog for myocardin 1 within a particular segment of chromosome 17 (Accession No. AC005358) and to determine the location of its exons and introns, enabling identification of the human cDNA sequence. The best EST match for myocardin 1 is Accession No. AI607474, for myocardin 2 is Accession No. BE311634, and for myocardin 3 is Accession No. AW500597.

The discovery of proteins that function to regulate cardiomyocyte growth and differentiation is important, both for advancing the basic understanding of heart development and to provide novel targets for the development of drugs and/or biotechnological methods to treat cardiac disease, for example by stimulating the growth

and differentiation of cells into cardiomyocytes after a patient has suffered tissue damage as a result of cardiomyopathy. Since myocardin appears to act as an early cardiac inducing factor with the capacity to induce cardiomyocyte development, and has the potential to reprogram cardiac fibroblasts, which constitute 40% of the cell types in the heart, to a cardiomyocyte type fate, it may be used in a variety of ways to directly treat cardiac disease and to develop additional treatments for cardiac disease. Further, because myocardin also appears to induce hypertrophy in cardiomyocytes, its overexpression may provide an additional benefit in the treatment of heart disease by, for example, improving the functioning of dysfunctional or malfuctional cardiomyocytes.

I. Nucleic Acids

In one aspect, the present invention provides nucleic acid sequences encoding cardiac cell regulatory factors designated myocardins. In a further aspect the coding sequence (as well as substantial non-coding protions) of a novel, N-terminally truncated cardiac-specific factor, designated herein as myocardin 1, is provided (SEQ ID NOS 1 and 25). In yet another aspect of the present invention, provided herein are nucleic acids encoding mouse and human myocardin 1, SEQ ID NOS: 29 and 27, respectively. The present invention is not limited in scope to any specific nucleic acid sequences disclosed herein as one of ordinary skill in the art could, using these nucleic acid sequences, readily identify related homologs, including, for example, homologs present in any of various species (*e.g.*, rat, rabbit, dog, monkey, gibbon, chimp, ape, baboon, cow, pig, horse, sheep, cat and other species).

As discussed below, a "myocardin nucleic acid sequence" may contain a variety of different bases and yet still produce a myocardin polypeptide according to the present invention. Such polypeptides will generally be functionally equivalent to, and/or structurally indistinguishable, from the human, mouse and other genes disclosed herein. Additionally, nucleic acid sequences encoding fragments of myocardin are provided herein. For example, fragments having increased activity (*e.g.*, the carboxy terminal fragments described in FIG. 6) as compared with the full-length myocardin polypeptide are described. Similarly, it will be readily recognized that fragments may be employed as probes, for example in the isolation of homologous sequences. Thus, as will be apparent

to those of skill in the art, fragments of the myocardin-encoding nucleic acid sequences as well as homologs thereof are likewise contemplated herein.

Similarly, any reference to a nucleic acid should be read as encompassing vectors and host cells containing that nucleic acid and, in some cases, capable of expressing the product of that nucleic acid. In addition to therapeutic considerations, cells expressing nucleic acids of the present invention may prove useful in the context of screening for agents that induce, repress, inhibit, augment, interfere with, block, abrogate, stimulate or enhance the function of myocardin.

A. Nucleic Acids Encoding Myocardin

Nucleic acids according to the present invention may encode an entire myocardin gene, a domain of myocardin, or any other fragment of myocardin as set forth herein. The nucleic acid may be derived from genomic DNA, *i.e.*, cloned directly from the genome of a particular organism. In preferred embodiments, however, the nucleic acid comprises complementary DNA (cDNA). Also contemplated is a cDNA plus a natural intron or an intron derived from another gene; such engineered molecules are sometime referred to as "mini-genes." At a minimum, these and other nucleic acids of the present invention may be used as molecular weight standards in, for example, gel electrophoresis.

The term "cDNA" is intended to refer to DNA prepared using messenger RNA (mRNA) as template. The advantage of using a cDNA, as opposed to genomic DNA or DNA polymerized from a genomic, non- or partially-processed RNA template, is that the cDNA primarily contains coding sequences of the corresponding protein. There may be times when the full or partial genomic sequence is preferred, such as where the non-coding regions are required for optimal expression or where non-coding regions such as introns are to be targeted in an antisense strategy.

It also is contemplated that a given myocardin polynucleotide may be represented by natural or synthetic variants that have slightly different nucleic acid sequences but, nonetheless, encode the same or homologous protein (see Table 1 below).

As used in this application, the term "a polynucleotide encoding a polypeptide" refers to a nucleic acid molecule that is isolated free of total cellular nucleic acid, including for example, a synthetic polynucleotide. In exemplary embodiments, the invention concerns a nucleic acid sequence essentially as set forth in SEQ ID NO: 1, SEQ ID NO: 25, SEQ ID NO: 27 or SEQ ID NO: 29. The term "comprises SEQ ID NO: 1 or 27" means that the nucleic acid sequence substantially corresponds to a portion of the aforementioned SEQ ID NO: 1 or 27 and likewise for other SEQ ID NOS providing nucleic acid sequences. The term "functionally equivalent codon" is used herein to refer to codons that encode the same amino acid, such as the six codons for arginine or serine (Table 1, below), and also refers to codons that encode biologically equivalent amino acids, as discussed in the following pages.

TABLE 1

Amino Acids			**Codons**
Alanine	Ala	A	GCA GCC GCG GCU
Cysteine	Cys	C	UGC UGU
Aspartic acid	Asp	D	GAC GAU
Glutamic acid	Glu	E	GAA GAG
Phenylalanine	Phe	F	UUC UUU
Glycine	Gly	G	GGA GGC GGG GGU
Histidine	His	H	CAC CAU
Isoleucine	Ile	I	AUA AUC AUU
Lysine	Lys	K	AAA AAG
Leucine	Leu	L	UUA UUG CUA CUC CUG CUU
Methionine	Met	M	AUG
Asparagine	Asn	N	AAC AAU
Proline	Pro	P	CCA CCC CCG CCU
Glutamine	Gln	Q	CAA CAG
Arginine	Arg	R	AGA AGG CGA CGC CGG CGU
Serine	Ser	S	AGC AGU UCA UCC UCG UCU
Threonine	Thr	T	ACA ACC ACG ACU
Valine	Val	V	GUA GUC GUG GUU
Tryptophan	Trp	W	UGG
Tyrosine	Tyr	Y	UAC UAU

Allowing for the degeneracy of the genetic code, sequences that have at least about 50%, usually at least about 60%, more usually about 70%, most usually about 80%, preferably at least about 90% and most preferably about 95% of nucleotides that are

identical to the nucleotides of a sequence set forth herein, for example SEQ ID NO: 1 or 27 are contemplated. Sequences that are essentially the same as those set forth in SEQ ID NO: 1 or 27 also may be functionally defined as sequences that are capable of hybridizing to a nucleic acid segment containing the complement of SEQ ID NO: 1 or 27 under standard conditions and likewise for other nucleotide sequences set forth herein.

The DNA segments of the present invention include those encoding biologically functional equivalent myocardin proteins, peptides and fragments thereof, as described elsewhere herein. Such sequences may arise as a consequence of codon redundancy and/or amino acid functional equivalency that are known to those of skill in the art. For example, polynucleotides encoding myocardin peptides analogous to the exemplary myocardin protein of SEQ ID NO: 2 or 28 are likewise contemplated herein. As discussed further below, and as known to those of skill in the art, various amino acid substitutions, deletions and/or additions may be made to a known amino acid sequence without adversely affecting the function and/or usefulness thereof. Alternatively, functionally equivalent proteins or peptides may be created via the application of recombinant DNA technology, in which changes in the protein structure may be engineered, based on considerations of the properties of the amino acids being exchanged. Changes designed by man may be introduced through the application of site-directed mutagenesis techniques or may be introduced randomly and screened later for the desired function, as described below.

B. Oligonucleotide Probes and Primers

Naturally, the present invention also encompasses DNA segments that are complementary, or essentially complementary, to the sequences set forth herein, for example in SEQ ID NO:1. Nucleic acid sequences that are "complementary" are those that are capable of base-pairing according to the standard Watson-Crick complementary rules. As used herein, the terms "complementary sequences" and "essentially complementary sequences" means nucleic acid sequences that are substantially complementary to, as may be assessed by the same nucleotide comparison set forth above, or are able to hybridize to a nucleic acid segment of one or more suequences set forth herein, for example SEQ ID NO:1 or 27, under relatively stringent conditions such as those described herein. Such sequences

may encode an entire myocardin protein or peptide or functional or non-functional fragments thereof.

The hybridizing segments may be short oligonucleotides. Sequences of 17 bases long should occur only once in the human genome and, therefore, suffice to specify a unique target sequence. Although shorter oligomers are easier to make and increase *in vivo* accessibility, numerous other factors are involved in determining the specificity of hybridization. Both binding affinity and sequence specificity of an oligonucleotide to its complementary target increases with increasing length. It is contemplated that exemplary oligonucleotides of 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100 or more base pairs will be used, although others are contemplated. Longer polynucleotides encoding 250, 500, 750, 1000, 1250, 1500, 2000, 2500, 3000 or 4000 bases and longer are contemplated as well. Such oligonucleotides will find use, for example, as probes in Southern and Northern blots and as primers in amplification reactions.

Suitable hybridization conditions will be well known to those of skill in the art. In certain applications, for example, substitution of amino acids by site-directed mutagenesis, it is appreciated that lower stringency conditions are required. Under these conditions, hybridization may occur even though the sequences of probe and target strand are not perfectly complementary, but are mismatched at one or more positions. Conditions may be rendered less stringent by increasing salt concentration and decreasing temperature. For example, a medium stringency condition could be provided by about 0.1 to 0.25 M NaCl at temperatures of about 37°C to about 55°C, while a low stringency condition could be provided by about 0.15 M to about 0.9 M salt, at temperatures ranging from about 20°C to about 55°C. Thus, hybridization conditions can be readily manipulated, and thus will generally be a method of choice depending on the desired results.

In other embodiments, hybridization may be achieved under conditions of, for example, 50 mM Tris-HCl (pH 8.3), 75 mm KCl, 3 mM $MgCl_2$, 10 mM dithiothreitol, at temperatures between approximately 20°C to about 37°C. Other hybridization conditions utilized could include approximately 10 mM Tris-HCl (pH 8.3), 50 mM KCl, 1.5 μM

$MgCl_2$, at temperatures ranging from approximately 40°C to about 72°C. Formamide and SDS also may be used to alter the hybridization conditions.

One method of using probes and primers of the present invention is in the search for genes related to myocardin proteins and peptides, including for example, myocardin proteins from other species. Normally, the target DNA will be a genomic or cDNA library, although screening may involve analysis of RNA molecules. By varying the stringency of hybridization, and the region of the probe, different degrees of homology may be discovered.

Another way of exploiting probes and primers of the present invention is in site-directed, or site-specific mutagenesis. Site-specific mutagenesis is a technique useful in the preparation of individual peptides, or biologically functional equivalent proteins or peptides, through specific mutagenesis of the underlying DNA. The technique further provides a ready ability to prepare and test sequence variants, incorporating one or more of the foregoing considerations, by introducing one or more nucleotide sequence changes into the DNA. Site-specific mutagenesis allows the production of mutants through the use of specific oligonucleotide sequences which encode the DNA sequence of the desired mutation, as well as a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on both sides of the deletion junction being traversed. Typically, a primer of about 17 to 25 nucleotides in length is preferred.

The technique typically employs a bacteriophage vector that exists in both a single stranded and double-stranded form. Typical vectors useful in site-directed mutagenesis include vectors such as the M13 phage. These phage vectors are commercially available and their use is generally well known to those skilled in the art. Double-stranded plasmids are also routinely employed in site-directed mutagenesis, which eliminates the step of transferring the gene of interest from a phage to a plasmid.

In general, site-directed mutagenesis is performed by first obtaining a single-stranded vector, or melting of two strands of a double-stranded vector which includes within its sequence a DNA sequence encoding the desired protein. An oligonucleotide

primer bearing the desired mutated sequence is synthetically prepared. This primer is then annealed with the single-stranded DNA preparation, taking into account the degree of mismatch when selecting hybridization conditions, and subjected to DNA polymerizing enzymes such as *E. coli* polymerase I Klenow fragment, in order to complete the synthesis of the mutation-bearing strand. Thus, a heteroduplex is formed wherein one strand encodes the original non-mutated sequence and the second strand bears the desired mutation. This heteroduplex vector is then used to transform appropriate cells, such as *E. coli* cells, and clones are selected that include recombinant vectors bearing the mutated sequence arrangement.

The preparation of sequence variants of the selected gene using site-directed mutagenesis is provided as a means of producing potentially useful species and is not meant to be limiting, as there are other ways in which sequence variants of genes may be obtained. For example, recombinant vectors encoding the desired gene may be treated with mutagenic agents, such as hydroxylamine, to obtain sequence variants.

C. Antisense Constructs

Antisense methodology takes advantage of the fact that nucleic acids tend to pair with "complementary" sequences. By complementary, it is meant that polynucleotides are those which are capable of base-pairing according to the standard Watson-Crick complementarity rules. That is, the larger purines will base pair with the smaller pyrimidines to form combinations of guanine paired with cytosine (G:C) and adenine paired with either thymine (A:T) in the case of DNA, or adenine paired with uracil (A:U) in the case of RNA. Inclusion of less common bases such as inosine, 5-methylcytosine, 6-methyladenine, hypoxanthine and others in hybridizing sequences does not interfere with pairing.

Targeting double-stranded (ds) DNA with polynucleotides leads to triple-helix formation; targeting RNA will lead to double-helix formation. Antisense polynucleotides, when introduced into a target cell, specifically bind to their target polynucleotide and interfere with transcription, RNA processing, transport, translation and/or stability. Antisense RNA constructs, or DNA encoding such antisense RNA's,

may be employed to inhibit gene transcription or translation or both within a host cell, either *in vitro* or *in vivo*, such as within a host animal, including a human subject.

Antisense constructs may be designed to bind to the promoter and/or other control regions, exons, introns or even exon-intron boundaries of a gene. It is contemplated that the most effective antisense constructs will include regions complementary to intron/exon splice junctions. Thus, it is proposed that a preferred embodiment includes an antisense construct with complementarity to regions within 50-200 bases of an intron-exon splice junction. It has been observed that some exon sequences can be included in the construct without seriously affecting the target selectivity thereof. The amount of exonic material included will vary depending on the particular exon and intron sequences used. One can readily test whether too much exon DNA is included simply by testing the constructs *in vitro* to determine whether normal cellular function is affected or whether the expression of related genes having complementary sequences is affected.

As stated above, "complementary" or "antisense" means polynucleotide sequences that are substantially complementary over their entire length and have very few base mismatches. For example, sequences of fifteen bases in length may be termed complementary when they have complementary nucleotides at thirteen or fourteen positions. Naturally, sequences which are completely complementary will be sequences which are entirely complementary throughout their entire length and have no base mismatches. Other sequences with lower degrees of homology also are contemplated. For example, an antisense construct which has limited regions of high homology, but also contains a non-homologous region (*e.g.*, ribozyme; see below) could be designed. These molecules, though having less than 50% homology, would bind to target sequences under appropriate conditions.

It may be advantageous to combine portions of genomic DNA with cDNA or synthetic sequences to generate specific constructs. For example, where an intron is desired in the ultimate construct, a genomic clone will need to be used. The cDNA or a synthesized polynucleotide may provide more convenient restriction sites for the

remaining portion of the construct and, therefore, would be used for the rest of the sequence.

D. Ribozymes

Although proteins traditionally have been used for catalysis of nucleic acids, another class of macromolecules has emerged as useful in this endeavor. Ribozymes are RNA-protein complexes that cleave nucleic acids in a site-specific fashion. Ribozymes have specific catalytic domains that possess endonuclease activity (Kim and Cook, 1987; Gerlach *et al.*, 1987; Forster and Symons, 1987). For example, a large number of ribozymes accelerate phosphoester transfer reactions with a high degree of specificity, often cleaving only one of several phosphoesters in an oligonucleotide substrate (Cook *et al.*, 1981; Michel and Westhof, 1990; Reinhold-Hurek and Shub, 1992). This specificity has been attributed to the requirement that the substrate bind via specific base-pairing interactions to the internal guide sequence ("IGS") of the ribozyme prior to chemical reaction.

Ribozyme catalysis has primarily been observed as part of sequence-specific cleavage/ligation reactions involving nucleic acids (Joyce, 1989; Cook *et al.*, 1981). For example, U.S. Patent 5,354,855 reports that certain ribozymes can act as endonucleases with a sequence specificity greater than that of known ribonucleases and approaching that of the DNA restriction enzymes. Thus, sequence-specific ribozyme-mediated inhibition of gene expression may be particularly suited to therapeutic applications (Scanlon *et al.*, 1991; Sarver *et al.*, 1990). Recently, it was reported that ribozymes elicited genetic changes in some cells lines to which they were applied; the altered genes included the oncogenes H-ras, c-fos and genes of HIV. Most of this work involved the modification of a target mRNA, based on a specific mutant codon that is cleaved by a specific ribozyme.

E. Vectors for Cloning, Gene Transfer and Expression

Within certain embodiments expression vectors are employed to express a myocardin polypeptide product, which can then be purified and, for example, be used to vaccinate animals to generate antisera or monoclonal antibody with which further studies

may be conducted. In other embodiments, the expression vectors are used in gene therapy. Expression requires that appropriate signals be provided in the vectors, including, for example, various regulatory elements, such as enhancers/promoters from viral and/or mammalian sources that are involved in driving expression of the genes of interest in host cells. Elements designed to optimize messenger RNA stability and translatability in host cells also can be used. The conditions for the use of a number of dominant drug selection markers for establishing permanent, stable cell clones expressing the products are also provided, as is an element that links expression of the drug selection markers to expression of the polypeptide.

(i) Regulatory Elements

Throughout this application, the term "expression construct" or “expression cassette” is meant to include any type of genetic construct containing a nucleic acid coding for a gene product in which part or all of the nucleic acid encoding sequence is capable of being transcribed. The transcript may be translated into a protein or polypeptide, but it need not be. In certain embodiments, expression includes both transcription of a gene and translation of mRNA into a gene product. In other embodiments, expression only includes transcription of the nucleic acid encoding a gene of interest.

As used herein, regulatory elements (or sequences) are nucleotide sequences that enhance or otherwise modulate transcription and/or translation or that stabilize transcription and/or translation products. Thus, for example, promoters operably linked to a coding sequence of an expression construct enhance transcription of that coding sequence and polyadenylation sequences operably linked to a coding sequence modulate polyadenylation of the gene transcript. Exemplary regulatory sequences can include, without limitation, promoters, enhancers, introns, termination sequences, polyadenylation sequences, stabilization sequences and the like.

In certain embodiments, the nucleic acid encoding a gene product is operably linked and under transcriptional control of a promoter. A "promoter" refers to a DNA sequence recognized by the synthetic machinery of the cell, or introduced synthetic

machinery, required to initiate the specific transcription of a gene. The phrase "under transcriptional control" means that the promoter is in the correct location and orientation in relation to the nucleic acid to control RNA polymerase initiation and expression of the gene.

The term promoter will be used here to refer to a group of transcriptional control modules that are clustered around the initiation site for RNA polymerase II. Much of the thinking about how promoters are organized derives from analyses of several viral promoters, including those for the HSV thymidine kinase (*tk*) and SV40 early transcription units. These studies, augmented by more recent work, have shown that promoters are typically composed of discrete functional modules, each consisting of approximately 7-20 bp of DNA, and containing one or more recognition sites for transcriptional activator or repressor proteins.

At least one module in each promoter functions to position the start site for RNA synthesis. The best known example of this is the TATA box, but in some promoters lacking a TATA box, such as the promoter for the mammalian terminal deoxynucleotidyl transferase gene and the promoter for the SV40 late genes, a discrete element overlying the start site itself helps to fix the place of initiation.

Additional promoter elements regulate the frequency of transcriptional initiation. Typically, these are located in the region 30-110 bp upstream of the start site, although a number of promoters have recently been shown to contain functional elements downstream of the start site as well. The spacing between promoter elements frequently is flexible, so that promoter function is preserved when elements are inverted or moved relative to one another. In the tk promoter, the spacing between promoter elements can be increased to 50 bp apart before activity begins to decline. Depending on the promoter, it appears that individual elements can function either co-operatively or independently to activate transcription.

In certain embodiments, the human cytomegalovirus (CMV) immediate early gene promoter, the SV40 early promoter, the Rous sarcoma virus (RSV) long terminal repeat, a human elongation factor (hEF) promoter, rat insulin promoter or

glyceraldehyde-3-phosphate dehydrogenase promoter can be used to obtain high-level expression of the coding sequence of interest. The use of other viral or mammalian cellular or bacterial phage promoters which are well known in the art to achieve expression of a coding sequence of interest is contemplated as well, provided that the levels of expression are sufficient for a given purpose.

By employing a promoter with well-known properties, the level and pattern of expression of the protein of interest following transfection or transformation can be optimized. By way of illustration, a ubiquitous, strong (*i.e.*, high activity) promoter may be employed to provide abundant gene expression in a group of host cells, or a tissue-specific promoter may be employed to target gene expression to one or more specific cell types. Further, selection of a promoter that is regulated in response to specific physiologic signals can permit inducible expression of the gene product. Tables 2 and 3 list several regulatory elements that may be employed, in the context of the present invention, to regulate the expression of the gene of interest. This list is not intended to be exhaustive of all the possible elements involved in the promotion of gene expression but, merely, to be exemplary thereof.

Enhancers are genetic elements that increase transcription from a promoter located at a distant position on the same molecule of DNA. Enhancers are organized much like promoters. That is, they are composed of many individual elements, each of which binds to one or more transcriptional proteins.

The basic distinction between enhancers and promoters is operational. An enhancer region as a whole is typically able to stimulate transcription at a distance; this need not be true of a promoter region or its component elements. On the other hand, a promoter typically has one or more elements that direct initiation of RNA synthesis at a particular site and in a particular orientation, whereas enhancers generally lack these specificities. Promoters and enhancers are often overlapping and contiguous, often seeming to have a very similar modular organization.

Tables 2 and 3, provided below, list several regulatory elements that may be employed, in the context of the present invention, to regulate the expression of the gene

of interest. This list is not intended to be exhaustive of all the possible elements involved in the promotion of gene expression but, merely, to be exemplary thereof. Other promoter/enhancer combinations (see, *e.g.*, the Eukaryotic Promoter Data Base EPDB) could also be used to drive expression of the gene. Eukaryotic cells can support cytoplasmic transcription from certain bacterial promoters if the appropriate bacterial polymerase is provided, either as part of the delivery complex or as an additional genetic expression construct.

TABLE 2

Promoter and/or Enhancer

Promoter/Enhancer	References
Immunoglobulin Heavy Chain	Banerji *et al.*, 1983; Gilles *et al.*, 1983; Grosschedl *et al.*, 1985; Atchinson *et al.*, 1986, 1987; Imler *et al.*, 1987; Weinberger *et al.*, 1984; Kiledjian *et al.*, 1988; Porton *et al.*; 1990
Immunoglobulin Light Chain	Queen *et al.*, 1983; Picard *et al.*, 1984
T-Cell Receptor	Luria *et al.*, 1987; Winoto *et al.*, 1989; Redondo *et al.*; 1990
HLA DQ a and/or DQ β	Sullivan *et al.*, 1987
β-Interferon	Goodbourn *et al.*, 1986; Fujita *et al.*, 1987; Goodbourn *et al.*, 1988
Interleukin-2	Greene *et al.*, 1989
Interleukin-2 Receptor	Greene *et al.*, 1989; Lin *et al.*, 1990
MHC Class II 5	Koch *et al.*, 1989
MHC Class II HLA-DRa	Sherman *et al.*, 1989
β-Actin	Kawamoto *et al.*, 1988; Ng *et al.*; 1989
Muscle Creatine Kinase (MCK)	Jaynes *et al.*, 1988; Horlick *et al.*, 1989; Johnson *et al.*, 1989
Human Elongation Factor-1A (hEF-1A or hEF-1α)	Uetsuki, *et al.*, 1989; Wakabayashi-Ito, *et al.*, 1994
Prealbumin (Transthyretin)	Costa *et al.*, 1988
Elastase I	Ornitz *et al.*, 1987
Metallothionein (MTII)	Karin *et al.*, 1987; Culotta *et al.*, 1989
Collagenase	Pinkert *et al.*, 1987; Angel *et al.*, 1987a

TABLE 2 Promoter and/or Enhancer	
Promoter/Enhancer	References
Albumin	Pinkert *et al.*, 1987; Tronche *et al.*, 1989, 1990
α-Fetoprotein	Godbout *et al.*, 1988; Campere *et al.*, 1989
t-Globin	Bodine *et al.*, 1987; Perez-Stable *et al.*, 1990
β-Globin	Trudel *et al.*, 1987
c-fos	Cohen *et al.*, 1987
c-HA-*ras*	Triesman, 1986; Deschamps *et al.*, 1985
Insulin	Edlund *et al.*, 1985
Neural Cell Adhesion Molecule (NCAM)	Hirsh *et al.*, 1990
α_1-Antitrypain	Latimer *et al.*, 1990
H2B (TH2B) Histone	Hwang *et al.*, 1990
Mouse and/or Type I Collagen	Ripe *et al.*, 1989
Glucose-Regulated Proteins (GRP94 and GRP78)	Chang *et al.*, 1989
Rat Growth Hormone	Larsen *et al.*, 1986
Human Serum Amyloid A (SAA)	Edbrooke *et al.*, 1989
Troponin I (TN I)	Yutzey *et al.*, 1989
Platelet-Derived Growth Factor (PDGF)	Pech *et al.*, 1989
Duchenne Muscular Dystrophy	Klamut *et al.*, 1990
SV40	Banerji *et al.*, 1981; Moreau *et al.*, 1981; Sleigh *et al.*, 1985; Firak *et al.*, 1986; Herr *et al.*, 1986; Imbra *et al.*, 1986; Kadesch *et al.*, 1986; Wang *et al.*, 1986; Ondek *et al.*, 1987; Kuhl *et al.*, 1987; Schaffner *et al.*, 1988
Polyoma	Swartzendruber *et al.*, 1975; Vasseur *et al.*, 1980; Katinka *et al.*, 1980, 1981; Tyndell *et al.*, 1981; Dandolo *et al.*, 1983; de Villiers *et al.*, 1984; Hen *et al.*, 1986; Satake *et al.*, 1988; Campbell and/or Villarreal, 1988

TABLE 2 Promoter and/or Enhancer	
Promoter/Enhancer	References
Retroviruses	Kriegler *et al.*, 1982, 1983; Levinson *et al.*, 1982; Kriegler *et al.*, 1983, 1984a, b, 1988; Bosze *et al.*, 1986; Miksicek *et al.*, 1986; Celander *et al.*, 1987; Thiesen *et al.*, 1988; Celander *et al.*, 1988; Choi *et al.*, 1988; Reisman *et al.*, 1989
Papilloma Virus	Campo *et al.*, 1983; Lusky *et al.*, 1983; Spandidos and/or Wilkie, 1983; Spalholz *et al.*, 1985; Lusky *et al.*, 1986; Cripe *et al.*, 1987; Gloss *et al.*, 1987; Hirochika *et al.*, 1987; Stephens *et al.*, 1987; Glue *et al.*, 1988
Hepatitis B Virus	Bulla *et al.*, 1986; Jameel *et al.*, 1986; Shaul *et al.*, 1987; Spandau *et al.*, 1988; Vannice *et al.*, 1988
Human Immunodeficiency Virus	Muesing *et al.*, 1987; Hauber *et al.*, 1988; Jakobovits *et al.*, 1988; Feng *et al.*, 1988; Takebe *et al.*, 1988; Rosen *et al.*, 1988; Berkhout *et al.*, 1989; Laspia *et al.*, 1989; Sharp *et al.*, 1989; Braddock *et al.*, 1989
Cytomegalovirus (CMV)	Weber *et al.*, 1984; Boshart *et al.*, 1985; Foecking *et al.*, 1986
Rous sarcoma virus (RSV)	Gorman, *et al.*, 1982; Guzman, *et al.*, 1993
Gibbon Ape Leukemia Virus	Holbrook *et al.*, 1987; Quinn *et al.*, 1989

TABLE 3 Inducible Elements		
Element	Inducer	References
MT II	Phorbol Ester (TFA) Heavy metals	Palmiter *et al.*, 1982; Haslinger *et al.*, 1985; Searle *et al.*, 1985; Stuart *et al.*, 1985; Imagawa *et al.*, 1987, Karin *et al.*, 1987; Angel *et al.*, 1987b; McNeall *et al.*, 1989
MMTV (mouse mammary tumor virus)	Glucocorticoids	Huang *et al.*, 1981; Lee *et al.*, 1981; Majors *et al.*, 1983; Chandler *et al.*, 1983; Lee *et al.*, 1984; Ponta *et al.*, 1985; Sakai *et al.*, 1988
β-Interferon	poly(rI)x poly(rc)	Tavernier *et al.*, 1983

TABLE 3 Inducible Elements		
Element	Inducer	References
Adenovirus 5 E2	ElA	Imperiale *et al.*, 1984
Collagenase	Phorbol Ester (TPA)	Angel *et al.*, 1987a
Stromelysin	Phorbol Ester (TPA)	Angel *et al.*, 1987b
SV40	Phorbol Ester (TPA)	Angel *et al.*, 1987b
Murine MX Gene	Interferon, Newcastle Disease Virus	Hug *et al.*, 1988
GRP78 Gene	A23187	Resendez *et al.*, 1988
α-2-Macroglobulin	IL-6	Kunz *et al.*, 1989
Vimentin	Serum	Rittling *et al.*, 1989
MHC Class I Gene H-2κb	Interferon	Blanar *et al.*, 1989
HSP70	ElA, SV40 Large T Antigen	Taylor *et al.*, 1989, 1990a, 1990b
Proliferin	Phorbol Ester-TPA	Mordacq *et al.*, 1989
Tumor Necrosis Factor	PMA	Hensel *et al.*, 1989
Thyroid Stimulating Hormone α Gene	Thyroid Hormone	Chatterjee *et al.*, 1989

In one aspect, tissue-specific promoters, *e.g.*, cardiac-specific and/or fibroblast-specific promoters, are of particular interest. By way of illustration, cardiac-specific promoters include the myosin light chain-2 promoter (Franz *et al.*, 1994; Kelly *et al.*, 1995), the alpha actin promoter (Moss *et al.*, 1996), the troponin 1 promoter (Bhavsar *et al.*, 1996); the Na^+/Ca^{2+} exchanger promoter (Barnes *et al.*, 1997), the dystrophin promoter (Kimura *et al.*, 1997), the creatine kinase promoter (Ritchie, M.E., 1996), the alpha7 integrin promoter (Ziober & Kramer, 1996), the brain natriuretic peptide promoter (LaPointe *et al.*, 1996) and the alpha B-crystallin/small heat shock protein promoter (Gopal-Srivastava, R., 1995), alpha myosin heavy chain promoter (Yamauchi-Takihara *et al.*, 1989) and the ANF promoter (LaPointe *et al.*, 1988).

Where a cDNA insert is employed, one will typically desire to include a polyadenylation signal to effect proper polyadenylation of the gene transcript. The nature of the polyadenylation signal is not believed to be crucial to the successful practice of the invention, and any such sequence may be employed such as human growth hormone and SV40 polyadenylation signals. Also contemplated as an element of the expression cassette is a terminator. These elements can serve to enhance message levels and to minimize read through from the cassette into other sequences.

(ii) Selectable Markers

In certain embodiments of the invention, in which cells contain nucleic acid constructs of the present invention, a cell may be identified *in vitro* or *in vivo* by including a marker in the expression construct. Such markers would confer an identifiable change to the cell permitting easy identification of cells containing the expression construct. Usually the inclusion of a drug selection marker aids in cloning and in the selection of transformants, for example, genes that confer resistance to neomycin, puromycin, hygromycin, DHFR, GPT, zeocin and histidinol are useful selectable markers. Alternatively, enzymes such as herpes simplex virus thymidine kinase (*tk*) or chloramphenicol acetyltransferase (CAT) may be employed. Immunologic markers also can be employed. The selectable marker employed is not believed to be important, so long as it is capable of being expressed simultaneously with the nucleic acid encoding a gene product. Further examples of selectable markers are well known to one of skill in the art.

(iii) Multigene Constructs and IRES

In certain embodiments of the invention, the use of internal ribosome entry site (IRES) elements are used to create multigene, or polycistronic, messages. IRES elements is believed to allow bypassing of the ribosome scanning model of 5′ methylated Cap dependent translation and facilitate translation at internal sites (Pelletier and Sonenberg, 1988). By way of illustration, IRES elements from two members of the picanovirus family (polio and encephalomyocarditis) have been described (Pelletier and Sonenberg, 1988), as well an IRES from a mammalian message (Macejak and Sarnow, 1991). IRES

elements can be linked to heterologous open reading frames. Multiple open reading frames can be transcribed together, each separated by an IRES, creating polycistronic messages. By virtue of the IRES element, each open reading frame is accessible to ribosomes for efficient translation. Multiple genes can be efficiently expressed using a single promoter/enhancer to transcribe a single message.

Any heterologous open reading frame can be linked to IRES elements. This includes genes for secreted proteins, multi-subunit proteins, encoded by independent genes, intracellular or membrane-bound proteins and selectable markers. In this way, expression of several proteins can be simultaneously engineered into a cell with a single construct and a single selectable marker.

(iv) Polyadenylation Signals

In expression, one will typically include a polyadenylation signal to effect proper polyadenylation of the transcript. The nature of the polyadenylation signal is not believed to be crucial to the successful practice of the invention, and any of a number of such sequences may be employed. Exemplary embodiments include the SV40 polyadenylation signal, the bovine growth hormone polyadenylation signal and others which are convenient and/or known to function well in various target cells. Also contemplated as an element of the expression cassette is a transcriptional termination site. These elements can serve to enhance message levels and/or to minimize read through from the cassette into other sequences.

(v) Vectors

The term “vector” is used to refer to carrier molecules with which a nucleic acid sequence can be associated for introduction into a cell. The nucleic acid sequence can be ”exogenous,” (*e.g.*, foreign to the cell into which it is introduced) or “endogenous” (*e.g.*, the same as a sequence in the cell into which it is introduced. Exemplary vectors include plasmids, cosmids, viruses (bacteriophage, animal viruses, and plant viruses), and artificial chromosomes (*e.g.,* YACs), lipid-based vectors (*e.g.*, liposomes) and other macromolecular complexes capable of mediating delivery of a polynucleotide to a host cell. One of skill in the art would be well equipped to construct a vector through standard

techniques, for example standard recombinant techniques such as described in Sambrook *et al.*, 1989 and Ausubel *et al.*, 1994, both incorporated herein by reference.

A large number of viral and non-viral vectors (including lipid-based and other synthetic delivery systems known in the art) can likewise be employed to deliver polynucleotides of the present invention. Such vectors may be modified, as known to those of skill in the art, to confer or enhance cell specificity. By way of illustration, the surface of viral vectors may be modified such that they preferentially or exclusively bind to and/or infect a particular target cell population.

As used herein, the term "expression vector" refers to a vector containing a nucleic acid sequence coding for at least part of a gene product capable of being transcribed. In some cases, the transcription product(s) are then translated into a protein, polypeptide, or peptide. In other cases, these sequences are not translated, for example, in the production of antisense molecules or ribozymes. Expression vectors can contain a variety of "control sequences," which refer to nucleic acid sequences that regulate the transcription and possibly translation of an operably linked coding sequence in a particular host organism. In addition to control sequences that govern transcription and translation, vectors and expression vectors may contain nucleic acid sequences that serve other functions as well for example as described infra.

(vi) Host Cells

As used herein, the terms "cell," "cell line," and "cell culture" may be used interchangeably. These terms also include their progeny, which is any and all subsequent generations. It is understood that all progeny may not be identical due to deliberate or inadvertent mutations. In the context of expressing a heterologous nucleic acid sequence, "host cell" refers to a prokaryotic or eukaryotic cell, and it includes any transformable organisms that is capable of replicating a vector and/or expressing a heterologous gene encoded by a vector. A host cell can, and has been, used as a recipient for vectors. A host cell may be "transfected" or "transformed," which refers to a process by which exogenous nucleic acid is transferred or introduced into the host cell. A transformed cell includes the primary subject cell and its progeny.

Some vectors may employ control sequences that allow it to be replicated and/or expressed in both prokaryotic and eukaryotic cells. One of skill in the art would further understand conditions under which to incubate such host cells to maintain them and to permit replication of a vector. Also understood and known are techniques and conditions that would allow large-scale production of vectors, as well as production of the nucleic acids encoded by vectors and their cognate polypeptides, proteins, or peptides.

(vii) Expression Systems

Numerous expression systems exist that comprise at least a part or all of the compositions discussed above. Prokaryote- and/or eukaryote-based systems can be employed for use with the present invention to produce nucleic acid sequences, or their cognate polypeptides, proteins and peptides. Many such systems are commercially and widely available.

The insect cell/baculovirus system can produce a high level of protein expression of a heterologous nucleic acid segment, such as described in U.S. Patent 5,871,986, 4,879,236, both herein incorporated by reference, and which can be bought, for example, under the name MAXBAC® 2.0 from INVITROGEN® and BACPACK™ baculovirus expression system from CLONTECH®.

Other examples of expression systems include STRATAGENE®'s COMPLETE CONTROL™ Inducible Mammalian Expression System, which involves a synthetic ecdysone-inducible receptor, or its pET Expression System, an E. coli expression system. Another example of an inducible expression system is available from INVITROGEN®, which carries the T-REX™ (tetracycline-regulated expression) System, an inducible mammalian expression system that uses the full-length CMV promoter. INVITROGEN® also provides a yeast expression system called the Pichia methanolica Expression System, which is designed for high-level production of recombinant proteins in the methylotrophic yeast Pichia methanolica. One of skill in the art would know how to express a vector, such as an expression construct, to produce a nucleic acid sequence or its cognate polypeptide, protein, or peptide.

(viii) Gene Delivery Means

There are a number of ways in which a gene of interest, for example within an expression vector, may be introduced into cells. In certain embodiments of the invention, the gene delivery means comprises a virus or engineered construct derived from a viral genome. The ability of certain viruses to enter cells for example via receptor-mediated endocytosis and to express viral genes stably and efficiently have made them attractive candidates for the transfer of foreign genes into mammalian cells (Ridgeway, 1988; Nicolas and Rubenstein, 1988; Baichwal and Sugden, 1986; Temin, 1986). The first viruses used as gene vectors were DNA viruses including the papovaviruses (simian virus 40, bovine papilloma virus, and polyoma) (Ridgeway, 1988; Baichwal and Sugden, 1986) and adenoviruses (Ridgeway, 1988; Baichwal and Sugden, 1986). Although these viral vectors generally have a relatively fixed capacity for foreign DNA can accommodate up to 5-10 kb of foreign DNA and many different viral vectors can be readily introduced into a variety of different cells and animals (see, *e.g.*, Nicolas and Rubenstein, 1988; Temin, 1986). Where viral vectors are employed to deliver the gene or genes of interest, it is generally preferred that they be replication-defective.

One of the preferred methods for *in vivo* gene delivery involves the use of an adenovirus expression vector. "Adenovirus expression vector" is meant to include those constructs containing adenovirus sequences sufficient to (a) support packaging of the construct and (b) to express polynucleotide that has been cloned therein. In this context, expression does not require that the gene product be synthesized.

An adenivorus expression vector comprises a genetically engineered form of adenovirus. Knowledge of the genetic organization of adenovirus, a linear, double-stranded DNA virus, allows substitution of large pieces of adenoviral DNA with foreign sequences (typically up to about 7 kB (Grunhaus and Horwitz, 1992)). Modified adenoviral and other viral vectors have also been constructed to provide for increased packaging capacity and are likewise contemplated herein. In contrast to retrovirus, the adenoviral infection of host cells does not generally result in chromosomal integration. Also, adenoviruses are structurally stable, and no genome rearrangement has been detected after extensive amplification. Adenovirus can infect various lineages of cells

regardless of their cell cycle stage. So far, adenoviral infection appears to be linked only to mild disease such as acute respiratory disease in humans.

Adenovirus is particularly suitable for use as a gene transfer vector because of its mid-sized genome, ease of manipulation, high titer, wide target cell range and high infectivity. In the case of adenovirus serotype 5 (Ad5), for example, both ends of the viral genome contain 100-200 base pair inverted repeats (ITRs), which are *cis* elements necessary for viral DNA replication and packaging. The early (E) and late (L) regions of the genome contain different transcription units that are divided by the onset of viral DNA replication. The E1 region (E1A and E1B) encodes proteins responsible for the regulation of transcription of the viral genome and a few cellular genes. The expression of the E2 region (E2A and E2B) results in the synthesis of the proteins for viral DNA replication. These proteins are involved in DNA replication, late gene expression and host cell shut-off (Renan, 1990). The products of the late genes, including the majority of the viral capsid proteins, are expressed only after significant processing of a single primary transcript issued by the major late promoter (MLP). The MLP (located at 16.8 m.u.) is particularly efficient during the late phase of infection, and the mRNA's issued from this promoter possess a 5'-tripartite leader (TPL) sequence which makes them preferred mRNA's for translation.

In one system, recombinant adenovirus is generated from homologous recombination between shuttle vector and provirus vector. Due to the possible recombination between two proviral vectors, wild-type adenovirus may be generated from this process. Therefore, it is important to minimize this possibility by reducing or eliminating adnoviral sequence overlaps within the system and/or to isolate a single clone of virus from an individual plaque and examine its genomic structure.

Generation and propagation of replication-deficient adenovirus vectors depend on a unique helper cell line, such as the human 293 cell line, which was transformed from human embryonic kidney cells by Adenovirus type 5 DNA fragments to constitutively expresses E1 proteins (Graham *et al.,* 1977). Since the E3 region is dispensable from the adenovirus genome (Jones and Shenk, 1978), the current adenovirus vectors, with the

help of 293 cells, generally carry foreign DNA in either the E1, the E3 or both regions (Graham and Prevec, 1991). In nature, adenovirus can package approximately 105% of the wild-type genome (Ghosh-Choudhury *et al.,* 1987), providing capacity for about 2 extra kb of DNA. Combined with the approximately 5.5 kb of DNA that is replaceable in the E1 and E3 regions, up to about 7.5 kb of foreign DNA may be packaged in an adenovirus. Additionally, modified adenoviral vectors are now available which have an even greater capacity to carry foreign DNA.

Helper cell lines may be derived from human cells such as human embryonic kidney cells, muscle cells, hematopoietic cells or other human embryonic mesenchymal or epithelial cells. Alternatively, the helper cells may be derived from the cells of other mammalian species that are permissive for human adenovirus. Such cells include, *e.g.,* Vero cells or other monkey embryonic mesenchymal or epithelial cells. As stated above, a preferred helper cell line is 293.

Racher *et al.* (1995) disclosed improved methods for culturing 293 cells and propagating adenovirus. In one format, natural cell aggregates are grown by inoculating individual cells into 1 liter siliconized spinner flasks (Techne, Cambridge, UK) containing 100-200 ml of medium. Following stirring at 40 rpm, the cell viability is estimated with trypan blue. In another format, Fibra-Cel microcarriers (Bibby Sterlin, Stone, UK) (5 g/l) are employed as follows. A cell inoculum, resuspended in 5 ml of medium, is added to the carrier (50 ml) in a 250 ml Erlenmeyer flask and left stationary, with occasional agitation, for 1 to 4 h. The medium is then replaced with 50 ml of fresh medium and shaking initiated. For virus production, cells are allowed to grow to about 80% confluence, after which time the medium is replaced (to 25% of the final volume) and adenovirus added at an MOI of 0.05. Cultures are left stationary overnight, following which the volume is increased to 100% and shaking commenced for another 72 h.

Other than the preference that the adenovirus vector be replication-defective, or at least conditionally defective, the nature of the adenovirus vector is not believed to be critical to the successful practice of the invention. The adenovirus may be selected from

any of the 42 different known serotypes or subgroups A-F. Adenovirus serotype 5 of subgroup C is a preferred starting material for obtaining a conditional replication-defective adenovirus vector for use in the present invention. This is, in part, because Adenovirus type 5 is a human adenovirus about which a great deal of biochemical and genetic information is known, and it has historically been used for most constructions employing adenovirus as a vector. Additionally, various modifications can be made to adenovirus to facilitate cell targeting of the expression cassette and/or otherwise modify vector interaction with the host cell. By way of illustration, it is known that primary fibroblasts generally express low levels of the high-affinity Coxsackie virus and Adenovirus receptor (CAR), which receptor facilitates transduction of host cells by the adenoviral vector. However, it is also known that adenoviral vectors can be modified, for example by altering the adenovirus fiber, to improve binding to other cell-surface receptors where CAR receptors are limited (see, *e.g.* Hidaka *et al.*, 1999).

As stated above, a preferred adenoviral vector according to the present invention lacks an adenovirus E1 region and thus, is replication defective. Typically, it is most convenient to introduce the polynucleotide encoding the gene of interest at the position from which the E1-coding sequences have been removed. However, the position of insertion of the construct within the adenovirus sequences is not critical to the invention. Further, other adenoviral sequences may be deleted and/or inactivated in addition to or in lieu of the E1 region. For example, the E2 and E4 regions are both necessary for adenoviral replication and thus may be modified to render an adenovirus vector replication-defective, in which case a helper cell line or helper virus complex may employed to provide such deleted/inactivated genes *in trans*. The polynucleotide encoding the gene of interest may alternatively be inserted in lieu of a deleted E3 region, such as in E3 replacement vectors as described by Karlsson *et al.* (1986), or in the E4 region where a helper cell line or helper virus complements an E4 defect. Other modifications are known to those of skill in the art and are likewise contemplated herein.

Adenovirus is easy to grow and manipulate and exhibits broad host range *in vitro* and *in vivo*. This group of viruses can be obtained in high titers, *e.g.,* 10^9-10^{12} plaque-forming units per ml, and they are highly infective. The life cycle of adenovirus does not

require integration into the host cell genome. The foreign genes delivered by adenovirus vectors are episomal and, therefore, have low genotoxicity to host cells. No side effects have been reported in studies of vaccination with wild-type adenovirus (Couch *et al.,* 1963; Top *et al.,* 1971), demonstrating their safety and therapeutic potential as *in vivo* gene transfer vectors.

Adenovirus vectors have been used in eukaryotic gene expression (Levrero *et al.,* 1991; Gomez-Foix *et al.,* 1992) and vaccine development (Grunhaus and Horwitz, 1992; Graham and Prevec, 1991). Animal studies initially suggested that recombinant adenovirus could be useful for gene therapy (see, *e.g.*, Stratford-Perricaudet and Perricaudet, 1991; Stratford-Perricaudet *et al.,* 1990; Rich *et al.,* 1993). Studies in administering recombinant adenovirus to different tissues include administration via intracoronary catheter into one or more coronary arteries of the heart (Hammond, *et al.*), U.S. Patents 5,792,453 and 6,100,242), trachea instillation (Rosenfeld *et al.,* 1991; Rosenfeld *et al.,* 1992), muscle injection (Ragot *et al.,* 1993), peripheral intravenous injections (Herz and Gerard, 1993) and stereotactic inoculation into the brain (Le Gal La Salle *et al.,* 1993).

The retroviruses are a group of single-stranded RNA viruses characterized by an ability to convert their RNA to double-stranded DNA in infected cells by a process of reverse-transcription (Coffin, 1990). The resulting DNA then stably integrates into cellular chromosomes as a provirus and directs synthesis of viral proteins. The integration results in the retention of the viral gene sequences in the recipient cell and its descendants. The retroviral genome contains three genes, gag, pol, and env that code for capsid proteins, polymerase enzyme, and envelope components, respectively. A sequence found upstream from the gag gene contains a signal for packaging of the genome into virions. Two long terminal repeat (LTR) sequences are present at the 5′ and 3′ ends of the viral genome. These contain strong promoter and enhancer sequences and are also required for integration in the host cell genome (Coffin, 1990).

In order to construct a retroviral vector, a nucleic acid encoding a gene of interest is inserted into the viral genome in the place of certain viral sequences to produce a virus

that is replication-defective. In order to produce virions, a packaging cell line containing the gag, pol, and env genes but without the LTR and packaging components is generally employed (Mann *et al.,* 1983). When a recombinant plasmid containing a cDNA, together with the retroviral LTR and packaging sequences is introduced into this cell line (by calcium phosphate precipitation for example), the packaging sequence allows the RNA transcript of the recombinant plasmid to be packaged into viral particles, which are then secreted into the culture media (Nicolas and Rubenstein, 1988; Temin, 1986; Mann *et al.,* 1983). The media containing the recombinant retroviruses is then collected, optionally concentrated, and used for gene transfer. Retroviral vectors are able to infect a broad variety of cell types. However, integration and stable expression require the division of host cells (Paskind *et al.,* 1975).

A novel approach designed to allow specific targeting of retrovirus vectors was recently developed based on the chemical modification of a retrovirus by the chemical addition of lactose residues to the viral envelope. This modification could permit the specific infection of hepatocytes via sialoglycoprotein receptors.

A different approach to targeting of recombinant retroviruses was designed in which biotinylated antibodies against a retroviral envelope protein and against a specific cell receptor were used. The antibodies were coupled via the biotin components by using streptavidin (Roux *et al.,* 1989). Using antibodies against major histocompatibility complex class I and class II antigens, they demonstrated the infection of a variety of human cells that bore those surface antigens with an ecotropic virus *in vitro* (Roux *et al.,* 1989).

There are certain limitations to the use of retrovirus. For example, retrovirus vectors usually integrate into random sites in the cell genome. This can lead to insertional mutagenesis through the interruption of host genes or through the insertion of viral regulatory sequences that can interfere with the function of flanking genes (Varmus *et al.,* 1981). Another concern with the use of defective retrovirus vectors is the potential appearance of wild-type replication-competent virus in the packaging cells. This can result from recombination events in which the intact-sequence from the recombinant

virus inserts upstream from the gag, pol, env sequence integrated in the host cell genome. However, new packaging cell lines are now available that should greatly decrease the likelihood of recombination (Markowitz *et al.,* 1988; Hersdorffer *et al.,* 1990).

Other viral vectors may be employed as expression constructs in the present invention. Vectors derived from viruses such as vaccinia virus (Ridgeway, 1988; Baichwal and Sugden, 1986; Coupar *et al.,* 1988) adeno-associated virus (AAV) (Ridgeway, 1988; Baichwal and Sugden, 1986; Hermonat and Muzycska, 1984) and herpesviruses may be employed. They offer several attractive features for various mammalian cells (Friedmann, 1989; Ridgeway, 1988; Baichwal and Sugden, 1986; Coupar *et al.,* 1988; Horwich *et al.,* 1990).

With the recent recognition of defective hepatitis B viruses, new insight was gained into the structure-function relationship of different viral sequences. *In vitro* studies showed that the virus could retain the ability for helper-dependent packaging and reverse transcription despite the deletion of up to 80% of its genome (Horwich *et al.,* 1990). This suggested that large portions of the genome could be replaced with foreign genetic material. The hepatotropism and persistence (integration) were particularly attractive properties for liver-directed gene transfer. Chang *et al.,* recently introduced the chloramphenicol acetyltransferase (CAT) gene into duck hepatitis B virus genome in the place of the polymerase, surface, and pre-surface coding sequences. It was co-transfected with wild-type virus into an avian hepatoma cell line. Culture media containing high titers of the recombinant virus were used to infect primary duckling hepatocytes. Stable CAT gene expression was detected for at least 24 days after transfection (Chang *et al.,* 1991).

In order to effect expression of sense or antisense gene constructs, the expression construct is delivered into a cell. This delivery may be accomplished *in vitro*, as in laboratory procedures for transforming cells lines, or *in vivo* or *ex vivo*, as in the treatment of certain disease states. One mechanism for delivery is via viral infection where the expression construct is encapsidated in an infectious viral particle.

Non-viral methods for the transfer of expression constructs into mammalian cells can also be used in the context of the present invention. These include calcium phosphate precipitation (Graham and Van Der Eb, 1973; Chen and Okayama, 1987; Rippe *et al.*, 1990) DEAE-dextran (Gopal, 1985), electroporation (Tur-Kaspa *et al.*, 1986; Potter *et al.*, 1984), direct microinjection (Harland and Weintraub, 1985), DNA-loaded liposomes (Nicolau and Sene, 1982; Fraley *et al.*, 1979) and lipofectamine-DNA complexes, cell sonication (Fechheimer *et al.,* 1987), gene bombardment using high velocity microprojectiles (Yang *et al.*, 1990), and receptor-mediated transfection (Wu and Wu, 1987; Wu and Wu, 1988). Some of these techniques may be successfully adapted for *in vivo* or *ex vivo* use.

Once the expression construct has been delivered into the cell the nucleic acid encoding the gene of interest may be positioned and expressed at different sites. In certain embodiments, the nucleic acid encoding the gene may be stably integrated into the genome of the cell. This integration may be in the cognate location and orientation via homologous recombination (gene replacement) or it may be integrated in a random, non-specific location (gene augmentation). In yet further embodiments, the nucleic acid may be stably maintained in the cell as a separate, episomal segment of DNA. Such nucleic acid segments or "episomes" encode sequences sufficient to permit maintenance and replication independent of or in synchronization with the host cell cycle. How the expression construct is delivered to a cell and where in the cell the nucleic acid remains is dependent on the type of expression construct employed.

In yet another embodiment of the invention, the expression construct may simply consist of naked recombinant DNA or plasmids. Transfer of the construct may be performed by any of the methods mentioned above which physically or chemically permeabilize the cell membrane. This is particularly applicable for transfer *in vitro* but it may be applied to *in vivo* use as well. Dubensky *et al.* (1984) successfully injected polyomavirus DNA in the form of calcium phosphate precipitates into liver and spleen of adult and newborn mice demonstrating active viral replication and acute infection. Benvenisty and Neshif (1986) also demonstrated that direct intraperitoneal injection of calcium phosphate-precipitated plasmids results in expression of the transfected genes. It

is envisioned that DNA encoding a gene of interest may also be transferred in a similar manner *in vivo* and express the gene product.

In still another embodiment of the invention, a naked DNA expression construct may be transferred into cells using particle bombardment. This method depends on the ability to accelerate DNA-coated microprojectiles to a high velocity allowing them to pierce cell membranes and enter cells without killing them (Klein *et al.,* 1987). Several devices for accelerating small particles have been developed. One such device relies on a high voltage discharge to generate an electrical current, which in turn provides the motive force (Yang *et al.,* 1990). The microprojectiles used have consisted of biologically inert substances such as tungsten or gold beads.

Selected organs including the liver, skin, and muscle tissue of rats and mice have been bombarded *in vivo* (Yang *et al.,* 1990; Zelenin *et al.,* 1991). This may require surgical exposure of the tissue or cells, to eliminate any intervening tissue between the gun and the target organ, *i.e., ex vivo* treatment. Again, DNA encoding a particular gene may be delivered via this method and still be incorporated by the present invention.

In a further embodiment of the invention, the expression construct may be complexed with one or more lipid components and/or entrapped in a liposome. Liposomes are vesicular structures characterized by a phospholipid bilayer membrane and an inner aqueous medium. Multilamellar liposomes have multiple lipid layers separated by aqueous medium. They form spontaneously when phospholipids are suspended in an excess of aqueous solution. The lipid components undergo self-rearrangement before the formation of closed structures and entrap water and dissolved solutes between the lipid bilayers (Ghosh and Bachhawat, 1991). Also contemplated are lipofectamine-DNA complexes.

Liposome-mediated nucleic acid delivery and expression of foreign DNA *in vitro* has been very successful. Wong *et al.,* (1980) demonstrated the feasibility of liposome-mediated delivery and expression of foreign DNA in cultured chick embryo, HeLa and hepatoma cells. Nicolau *et al.,* (1987) accomplished successful liposome-mediated gene transfer in rats after intravenous injection.

In certain embodiments of the invention, the liposome may be complexed with a hemagglutinating virus (HVJ). This has been shown to facilitate fusion with the cell membrane and promote cell entry of liposome-encapsulated DNA (Kaneda *et al.,* 1989). In other embodiments, the liposome may be complexed or employed in conjunction with nuclear non-histone chromosomal proteins (HMG-1) (Kato *et al.,* 1991). In yet further embodiments, the liposome may be complexed or employed in conjunction with both HVJ and HMG-1. In that such expression constructs have been successfully employed in transfer and expression of nucleic acid *in vitro* and *in vivo*, then they are applicable for the present invention. Where a bacterial promoter is employed in the DNA construct, it also will be desirable to include within the liposome an appropriate bacterial polymerase.

Other expression constructs which can be employed to deliver a nucleic acid encoding a particular gene into cells are receptor-mediated delivery vehicles. These take advantage of the selective uptake of macromolecules by receptor-mediated endocytosis in most eukaryotic cells. Because of the cell type-specific distribution of various receptors, the delivery can be highly specific (Wu and Wu, 1993).

Receptor-mediated gene targeting vehicles generally consist of two components: a cell receptor-specific ligand and a DNA-binding agent. Several ligands have been used for receptor-mediated gene transfer. The most extensively characterized ligands are asialoorosomucoid (ASOR) (Wu and Wu, 1987) and transferrin (Wagner *et al.,* 1990). Recently, a synthetic neoglycoprotein, which recognizes the same receptor as ASOR, has been used as a gene delivery vehicle (Ferkol *et al.,* 1993; Perales *et al.,* 1994) and epidermal growth factor (EGF) has also been used to deliver genes to squamous carcinoma cells (Myers, EPO 0273085).

In other embodiments, the delivery vehicle may comprise a ligand and a liposome. For example, Nicolau *et al.,* (1987) employed lactosyl-ceramide, a galactose-terminal asialganglioside, incorporated into liposomes and observed an increase in the uptake of the insulin gene by hepatocytes. Thus, it is feasible that a nucleic acid encoding a particular gene also may be specifically delivered into a cell type by any number of receptor-ligand systems with or without liposomes. For example, epidermal

growth factor (EGF) may be used as the receptor for mediated delivery of a nucleic acid into cells that exhibit upregulation of EGF receptor. Mannose can be used to target the mannose receptor on liver cells. Also, antibodies to CD5 (CLL), CD22 (lymphoma), CD25 (T-cell leukemia) and MAA (melanoma) can similarly be used as targeting moieties.

In certain embodiments, gene transfer may more easily be performed under *ex vivo* conditions. *Ex vivo* gene therapy refers to the isolation of cells from an animal, the delivery of a nucleic acid into the cells *in vitro*, and then the return of the modified cells back into an animal. This may involve the surgical removal of tissue/organs from an animal or the primary culture of cells and tissues.

II. Myocardin Peptides and Polypeptides

The present invention also provides exemplary myocardin protein/polypeptide sequences. For example, SEQ ID NOS:2, 26, 28 and 30 provide amino acid sequences for myocardins of SEQ ID NOS:1, 25, 27 and 29, respectively. In addition to entire myocardin molecules, the present invention also relates to fragments of the polypeptides that may or may not retain the various functions described below. By way of illustration, N-terminally truncated myocardin 1 polypeptides from mouse and human (SEQ ID NOS: 2 and 26, respectively) are provided, which polypeptides retain the various functions described below. Fragments, including the N-terminus of the molecule may be generated by genetic engineering of translation stop sites within the coding region (discussed below). Alternatively, treatment of the polypeptides with proteolytic enzymes, known as proteases, can produces a variety of N-terminal, C-terminal and internal fragments. These fragments may be purified according to known methods, such as precipitation (*e.g.*, ammonium sulfate), HPLC, ion exchange chromatography, affinity chromatography (including immunoaffinity chromatography) or various size separations (sedimentation, gel electrophoresis, gel filtration).

A. Structural and Functional Aspects

Myocardin 1 from human and mouse, shown in SEQ ID NO:28 and SEQ ID NO:30 are 935 and 938 residues, respectively. In human myocardin 1, the nuclear

localization sequence (NLS) is located between residues 245 and 254, within a basic region at residues 243-260. A glutamine-rich (Q) domain is located between residues 287-320. The SAP domain is found at residues 380-414. The transcription activation domain is located at the carboxyl-terminus at 670 to 935.

In general, myocardins are cell regulatory proteins/peptides that function to modulate cell phenotype. In particular, myocardin can be used to reduce the deleterious effects of non-cardiomyocytes on injured myocardium and/or to stimulate non-cardiomyocytes to perform one or more functions typical of cardiomyocytes, thereby enhancing cardiac function. By way of illustration, myocardin 1 is a novel cardiac-specific regulatory protein capable of modulating the phenotype of target cells within the heart, such as fibroblasts. Overexpression of myocardin 1 in fibroblasts is sufficient to activate expression of a variety of cardiac promoters, including α-myosin heavy chain, atrial natriuretic factor, Nkx2.5 and SM22. In combination with GATA4, myocardin 1 transactivates regulatory sequences in the cardiac specific homeobox Nkx2.5 gene. In addition myocardin 1 is a potent inhibitor of cell proliferation, demonstrated by a reduced number of transfected cells expressing myocardin 1 compared to those expressing a control marker gene. Further, though inhibitory of cell proliferation, myocardin appears to stimulate cardiomyocyte hypertrophy. These results may provide an explanation for the post-mitotic feautures of the cardiomyocytes.

B. Variants of Myocardin

Amino acid sequence variants of a myocardin polypeptide can be substitutional, insertional or deletion variants. Deletion variants lack one or more residues of the native protein which are not essential for function or immunogenic activity, and are exemplified by the variants lacking a transmembrane sequence described above. Another common type of deletion variant is one lacking secretory signal sequences or signal sequences directing a protein to bind to a particular part of a cell. Insertional mutants typically involve the addition of material at a non-terminal point in the polypeptide. This may include the insertion of an immunoreactive epitope or simply a single residue. Terminal additions, called fusion proteins, are discussed below.

Substitutional variants typically contain the exchange of one amino acid for another at one or more sites within the protein, and may be designed to modulate one or more properties of the polypeptide, such as stability against proteolytic cleavage, without the loss of other functions or properties. Substitutions of this kind preferably are conservative, that is, one amino acid is replaced with one of similar shape and charge. Conservative substitutions are well known in the art and include, for example, the changes of: alanine to serine; arginine to lysine; asparagine to glutamine or histidine; aspartate to glutamate; cysteine to serine; glutamine to asparagine; glutamate to aspartate; glycine to proline; histidine to asparagine or glutamine; isoleucine to leucine or valine; leucine to valine or isoleucine; lysine to arginine; methionine to leucine or isoleucine; phenylalanine to tyrosine, leucine or methionine; serine to threonine; threonine to serine; tryptophan to tyrosine; tyrosine to tryptophan or phenylalanine; and valine to isoleucine or leucine.

The following is a discussion based upon changing of the amino acids of a protein to create an equivalent, or even an improved, second-generation molecule. For example, certain amino acids may be substituted for other amino acids in a protein structure without appreciable loss of interactive binding capacity with structures such as, for example, antigen-binding regions of antibodies or binding sites on substrate molecules. Since it is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid substitutions can be made in a protein sequence, and its underlying DNA coding sequence, and nevertheless obtain a protein with like properties. It is thus contemplated by the inventors that various changes may be made in the DNA sequences of genes without appreciable loss of their biological utility or activity, as discussed below. Table 1 shows the codons that encode particular amino acids.

In making such changes, the hydropathic index of amino acids may be considered. The importance of the hydropathic amino acid index in conferring interactive biologic function on a protein is generally understood in the art (Kyte and Doolittle, 1982). It is accepted that the relative hydropathic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines the interaction of the protein with other molecules, for example, enzymes, substrates, receptors, DNA, antibodies, antigens, and the like.

Each amino acid has been assigned a hydropathic index on the basis of their hydrophobicity and charge characteristics (Kyte and Doolittle, 1982), these are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (-0.4); threonine (-0.7); serine (-0.8); tryptophan (-0.9); tyrosine (-1.3); proline (-1.6); histidine (-3.2); glutamate (-3.5); glutamine (-3.5); aspartate (-3.5); asparagine (-3.5); lysine (-3.9); and arginine (-4.5).

It is known in the art that certain amino acids may be substituted by other amino acids having a similar hydropathic index or score and still result in a protein with similar biological activity, *i.e.*, still obtain a biological functionally equivalent protein. In making such changes, the substitution of amino acids whose hydropathic indices are within ±2 is preferred, those which are within ±1 are particularly preferred, and those within ±0.5 are even more particularly preferred.

It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U.S. Patent 4,554,101, incorporated herein by reference, states that the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with a biological property of the protein. As detailed in U.S. Patent 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0 ± 1); glutamate (+3.0 ± 1); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (-0.4); proline (-0.5 ± 1); alanine (-0.5); histidine *-0.5); cysteine (-1.0); methionine (-1.3); valine (-1.5); leucine (-1.8); isoleucine (-1.8); tyrosine (-2.3); phenylalanine (-2.5); tryptophan (-3.4).

It is understood that an amino acid can be substituted for another having a similar hydrophilicity value and still obtain a biologically equivalent and immunologically equivalent protein. In such changes, the substitution of amino acids whose hydrophilicity values are within ±2 is preferred, those that are within ±1 are particularly preferred, and those within ±0.5 are even more particularly preferred.

As outlined above, amino acid substitutions are generally based on the relative similarity of the amino acid side-chain substituents, for example, their hydrophobicity,

hydrophilicity, charge, size, and the like. Exemplary substitutions that take various of the foregoing characteristics into consideration are well known to those of skill in the art and include: arginine and lysine; glutamate and aspartate; serine and threonine; glutamine and asparagine; and valine, leucine and isoleucine.

Another embodiment for the preparation of polypeptides according to the invention is the use of peptide mimetics. Mimetics are peptide-containing molecules that mimic elements of protein secondary structure (Johnson *et al,* 1993). The underlying rationale behind the use of peptide mimetics is that the peptide backbone of proteins exists chiefly to orient amino acid side chains in such a way as to facilitate molecular interactions, such as those of antibody and antigen. A peptide mimetic is expected to permit molecular interactions similar to the natural molecule. These principles may be used, in conjunction with the principles outline above, to engineer second generation molecules having many of the natural properties of myocardin, but with altered and even improved characteristics.

C. Domain Switching

Domain switching involves the generation of chimeric molecules using different but, in this case, related polypeptides. By comparing various myocardin proteins, one can make predictions as to the functionally significant regions of these molecules. It is possible, then, to switch related domains of these molecules in an effort to determine the criticality of these regions to myocardin function. These molecules may have additional value in that these "chimeras" can be distinguished from natural molecules, while possibly providing the same function. In particular, it is contemplated that one will create chimeras between myocardins, for example, between myocardin 1 & myocardin 2, myocardin1 & myocardin 3, myocardin 2 & myocardin 3, and/or myocardin 1, myocardin 2 & myocardin 3.

D. Fusion Proteins

A specialized kind of insertional variant is the fusion protein. This molecule generally has all or a substantial portion of the native molecule linked, at the N- or C-terminus, to all or a portion of a second polypeptide. For example, fusions typically employ leader sequences from other species to permit the recombinant expression of a protein in a heterologous host. Another useful fusion includes the addition of a immunologically active domain, such as an antibody epitope, to facilitate purification of the fusion protein. Inclusion of a cleavage site at or near the fusion junction will facilitate removal of the extraneous polypeptide after purification. Other useful fusions include linking of functional domains, such as active sites from enzymes, glycosylation domains, cellular targeting signals or transmembrane regions.

E. Purification of Proteins

It may be desirable to purify myocardin or variants thereof. Protein purification techniques are well known to those of skill in the art. These techniques involve, at one level, the crude fractionation of the cellular milieu to polypeptide and non-polypeptide fractions. Having separated the polypeptide from other proteins, the polypeptide of interest may be further purified using chromatographic and electrophoretic techniques to achieve partial or complete purification (or purification to homogeneity). Analytical methods particularly suited to the preparation of a pure peptide are ion-exchange chromatography, exclusion chromatography; polyacrylamide gel electrophoresis; isoelectric focusing. A particularly efficient method of purifying peptides is fast protein liquid chromatography or even HPLC.

Certain aspects of the present invention concern the purification, and in particular embodiments, the substantial purification, of an encoded protein or peptide. The term "purified protein or peptide" as used herein, is intended to refer to a composition, isolatable from other components, wherein the protein or peptide is purified to any degree relative to its naturally-obtainable state. A purified protein or peptide therefore also refers to a protein or peptide, free from the environment in which it may naturally occur.

Generally, "purified" will refer to a protein or peptide composition that has been subjected to fractionation to remove various other components, and which composition substantially retains its expressed biological activity. Where the term "substantially purified" is used, this designation will refer to a composition in which the protein or peptide forms the major component of the composition, such as constituting about 50%, about 60%, about 70%, about 80%, about 90%, about 95% or more of the proteins in the composition.

Various methods for quantifying the degree of purification of the protein or peptide will be known to those of skill in the art in light of the present disclosure. These include, for example, determining the specific activity of an active fraction, or assessing the amount of polypeptides within a fraction by SDS/PAGE analysis. A preferred method for assessing the purity of a fraction is to calculate the specific activity of the fraction, to compare it to the specific activity of the initial extract, and to thus calculate the degree of purity, herein assessed by a "-fold purification number." The actual units used to represent the amount of activity will, of course, be dependent upon the particular assay technique chosen to follow the purification and whether or not the expressed protein or peptide exhibits a detectable activity.

Various techniques suitable for use in protein purification will be well known to those of skill in the art. These include, for example, precipitation with ammonium sulphate, PEG, antibodies and the like or by heat denaturation, followed by centrifugation; chromatography steps such as ion exchange, gel filtration, reverse phase, hydroxylapatite and affinity chromatography; isoelectric focusing; gel electrophoresis; and combinations of such and other techniques. As is generally known in the art, it is believed that the order of conducting the various purification steps may be changed, or that certain steps may be omitted, and still result in a suitable method for the preparation of a substantially purified protein or peptide.

There is no general requirement that the protein or peptide always be provided in their most purified state. Indeed, it is contemplated that less substantially purified products will have utility in certain embodiments. Partial purification may be

accomplished by using fewer purification steps in combination, or by utilizing different forms of the same general purification scheme. For example, it is appreciated that a cation-exchange column chromatography performed utilizing an HPLC apparatus will generally result in a greater "-fold" purification than the same technique utilizing a low pressure chromatography system. Methods exhibiting a lower degree of relative purification may have advantages in total recovery of protein product, or in maintaining the activity of an expressed protein.

It is known that the migration of a polypeptide can vary, sometimes significantly, with different conditions of SDS/PAGE (Capaldi *et al.,* 1977). It will therefore be appreciated that under differing electrophoresis conditions, the apparent molecular weights of purified or partially purified expression products may vary.

High Performance Liquid Chromatography (HPLC) is characterized by a very rapid separation with extraordinary resolution of peaks. This is achieved by the use of very fine particles and high pressure to maintain an adequate flow rate. Separation can be accomplished in a matter of minutes, or at most an hour. Moreover, only a very small volume of the sample is needed because the particles are so small and close-packed that the void volume is a very small fraction of the bed volume. Also, the concentration of the sample need not be very great because the bands are so narrow that there is very little dilution of the sample.

Gel chromatography, or molecular sieve chromatography, is a special type of partition chromatography that is based on molecular size. The theory behind gel chromatography is that the column, which is prepared with tiny particles of an inert substance that contain small pores, separates larger molecules from smaller molecules as they pass through or around the pores, depending on their size. As long as the material of which the particles are made does not adsorb the molecules, the sole factor determining rate of flow is the size. Hence, molecules are eluted from the column in decreasing size, so long as the shape is relatively constant. Gel chromatography is unsurpassed for separating molecules of different size because separation is independent of other factors

such as pH, ionic strength, temperature, *etc.* There also is virtually no adsorption, less zone spreading and the elution volume is related in a simple matter to molecular weight.

Affinity Chromatography is a chromatographic procedure that relies on the specific affinity between a substance to be isolated and a molecule that it can specifically bind to. This is a receptor-ligand type interaction. The column material is synthesized by covalently coupling one of the binding partners to an insoluble matrix. The column material is then able to specifically adsorb the substance from the solution. Elution occurs by changing the conditions to those in which binding will not occur (alter pH, ionic strength, temperature, *etc.*).

A particular type of affinity chromatography useful in the purification of carbohydrate containing compounds is lectin affinity chromatography. Lectins are a class of substances that bind to a variety of polysaccharides and glycoproteins. Lectins are usually coupled to agarose by cyanogen bromide. Conconavalin A coupled to Sepharose was the first material of this sort to be used and has been widely used in the isolation of polysaccharides and glycoproteins other lectins that have been include lentil lectin, wheat germ agglutinin which has been useful in the purification of N-acetyl glucosaminyl residues and *Helix pomatia* lectin. Lectins themselves are purified using affinity chromatography with carbohydrate ligands. Lactose has been used to purify lectins from castor bean and peanuts; maltose has been useful in extracting lectins from lentils and jack bean; N-acetyl-D galactosamine is used for purifying lectins from soybean; N-acetyl glucosaminyl binds to lectins from wheat germ; D-galactosamine has been used in obtaining lectins from clams and L-fucose will bind to lectins from lotus.

The matrix should be a substance that itself does not adsorb molecules to any significant extent and that has a broad range of chemical, physical and thermal stability. The ligand should be coupled in such a way as to not affect its binding properties. The ligand should also provide relatively tight binding. And it should be possible to elute the substance without destroying the sample or the ligand. One of the most common forms of affinity chromatography is immunoaffinity chromatography. The generation of

antibodies that would be suitable for use in accord with the present invention is discussed below.

F. Synthetic Peptides

The present invention also includes smaller myocardin-related peptides for use in various embodiments of the present invention. Because of their relatively small size, the peptides of the invention can also be synthesized in solution or on a solid support in accordance with conventional techniques. Various automatic synthesizers are commercially available and can be used in accordance with known protocols. See, for example, Stewart and Young (1984); Tam *et al.* (1983); Merrifield (1986); and Barany and Merrifield (1979), each incorporated herein by reference. Short peptide sequences, or libraries of overlapping peptides, usually from about 6 up to about 35 to 50 amino acids, which correspond to the selected regions described herein, can be readily synthesized and then screened in screening assays designed to identify reactive peptides. Alternatively, recombinant DNA technology may be employed wherein a nucleotide sequence which encodes a peptide of the invention is inserted into an expression vector, transformed or transfected into an appropriate host cell and cultivated under conditions suitable for expression.

G. Antigen Compositions

The present invention also provides for the use of myocardin proteins or peptides as antigens for the immunization of animals relating to the production of antibodies. It is envisioned that myocardin or portions thereof, will be coupled, bonded, bound, conjugated or chemically-linked to one or more agents via linkers, polylinkers or derivatized amino acids. This may be performed such that a bispecific or multivalent composition or vaccine is produced. It is further envisioned that the methods used in the preparation of these compositions will be familiar to those of skill in the art and should be suitable for administration to animals, *i.e.*, pharmaceutically acceptable. Preferred agents are the carriers are keyhole limpet hemocyannin (KLH) or bovine serum albumin (BSA).

III. Generating Antibodies Reactive With Myocardin

In another aspect, the present invention contemplates an antibody that is immunoreactive with a myocardin molecule of the present invention, or any portion thereof. An antibody can be a polyclonal or a monoclonal antibody. In a preferred embodiment, an antibody is a monoclonal antibody. Means for preparing and characterizing antibodies are well known in the art (see, *e.g.*, Harlow and Lane, 1988).

Briefly, a polyclonal antibody is prepared by immunizing an animal with an immunogen comprising a polypeptide of the present invention and collecting antisera from that immunized animal. A wide range of animal species can be used for the production of antisera. Typically an animal used for production of anti-antisera is a non-human animal including rabbits, mice, rats, hamsters, pigs or horses. Because of the relatively large blood volume of rabbits, a rabbit is a preferred choice for production of polyclonal antibodies.

Antibodies, both polyclonal and monoclonal, specific for isoforms of antigen may be prepared using conventional immunization techniques, as will be generally known to those of skill in the art. A composition containing antigenic epitopes of the compounds of the present invention can be used to immunize one or more experimental animals, such as a rabbit or mouse, which will then proceed to produce specific antibodies against the compounds of the present invention. Polyclonal antisera may be obtained, after allowing time for antibody generation, simply by bleeding the animal and preparing serum samples from the whole blood.

It is proposed that the monoclonal antibodies of the present invention will find useful application in standard immunochemical procedures, such as ELISA and Western blot methods and in immunohistochemical procedures such as tissue staining, as well as in other procedures which may utilize antibodies specific to myocardin-related antigen epitopes. Additionally, it is proposed that monoclonal antibodies specific to the particular myocardin of different species may be utilized in other useful applications

In general, both polyclonal and monoclonal antibodies against myocardin may be used in a variety of embodiments. For example, they may be employed in antibody

cloning protocols to obtain cDNAs or genes encoding other myocardin. They may also be used in inhibition studies to analyze the effects of myocardin-related peptides in cells or animals. Myocardin antibodies will also be useful in immunolocalization studies to analyze the distribution of myocardins during various cellular events, for example, to determine the cellular or tissue-specific distribution of myocardin polypeptides at different points in the cell cycle. A particularly useful application of such antibodies is in purifying native or recombinant myocardin, for example, using an antibody affinity column. The operation of such immunological techniques will be known to those of skill in the art in light of the present disclosure.

Means for preparing and characterizing antibodies are well known in the art (see, *e.g.*, Harlow and Lane, 1988; incorporated herein by reference). More specific examples of monoclonal antibody preparation are given in the examples below.

As is well known in the art, a given composition may vary in its immunogenicity. It is often necessary therefore to boost the host immune system, as may be achieved by coupling a peptide or polypeptide immunogen to a carrier. Exemplary and preferred carriers are keyhole limpet hemocyanin (KLH) and bovine serum albumin (BSA). Other albumins such as ovalbumin, mouse serum albumin or rabbit serum albumin can also be used as carriers. Means for conjugating a polypeptide to a carrier protein are well known in the art and include glutaraldehyde, *m*-maleimidobencoyl-N-hydroxysuccinimide ester, carbodiimide and bis-biazotized benzidine.

As also is well known in the art, the immunogenicity of a particular immunogen composition can be enhanced by the use of non-specific stimulators of the immune response, known as adjuvants. Exemplary and preferred adjuvants include complete Freund's adjuvant (a non-specific stimulator of the immune response containing killed *Mycobacterium tuberculosis)*, incomplete Freund's adjuvants and aluminum hydroxide adjuvant.

The amount of immunogen composition used in the production of polyclonal antibodies varies upon the nature of the immunogen as well as the animal used for immunization. A variety of routes can be used to administer the immunogen

(subcutaneous, intramuscular, intradermal, intravenous and intraperitoneal). The production of polyclonal antibodies may be monitored by sampling blood of the immunized animal at various points following immunization. A second, booster, injection may also be given. The process of boosting and titering is repeated until a suitable titer is achieved. When a desired level of immunogenicity is obtained, the immunized animal can be bled and the serum isolated and stored, and/or the animal can be used to generate mAbs.

MAbs may be readily prepared through use of well-known techniques, such as those exemplified in U.S. Patent 4,196,265, incorporated herein by reference. Typically, this technique involves immunizing a suitable animal with a selected immunogen composition, *e.g.*, a purified or partially purified MCIP protein, polypeptide or peptide or cell expressing high levels of MCIP. The immunizing composition is administered in a manner effective to stimulate antibody producing cells. Rodents such as mice and rats are preferred animals, however, the use of rabbit, sheep frog cells is also possible. The use of rats may provide certain advantages (Goding, 1986), but mice are preferred, with the BALB/c mouse being most preferred as this is most routinely used and generally gives a higher percentage of stable fusions.

IV. Immunologic Analysis

The use of antibodies of the present invention, in an ELISA assay is contemplated. For example, anti-myocardin antibodies are immobilized onto a selected surface, preferably a surface exhibiting a protein affinity such as the wells of a polystyrene microtiter plate. After washing to remove incompletely adsorbed material, it is desirable to bind or coat the assay plate wells with a non-specific protein that is known to be antigenically neutral with regard to the test antisera such as bovine serum albumin (BSA), casein or solutions of powdered milk. This allows for blocking of non-specific adsorption sites on the immobilizing surface and thus reduces the background caused by non-specific binding of antigen onto the surface.

After binding of antibody to the well, coating with a non-reactive material to reduce background, and washing to remove unbound material, the immobilizing surface

is contacted with the sample to be tested in a manner conducive to immune complex (antigen/antibody) formation.

Following formation of specific immunocomplexes between the test sample and the bound antibody, and subsequent washing, the occurrence and even amount of immunocomplex formation may be determined by subjecting same to a second antibody having specificity for myocardin or a fragment thereof that differs from the first antibody. Appropriate conditions preferably include diluting the sample with diluents such as BSA, bovine gamma globulin (BGG) and phosphate buffered saline (PBS)/Tween®. These added agents also tend to assist in the reduction of nonspecific background. The layered antisera is then allowed to incubate for from about 2 to about 4 hr, at temperatures preferably on the order of about 25° to about 27°C. Following incubation, the antisera-contacted surface is washed so as to remove non-immunocomplexed material. A preferred washing procedure includes washing with a solution such as PBS/Tween®, or borate buffer.

To provide a detecting means, the second antibody will preferably have an associated enzyme that will generate a color development upon incubating with an appropriate chromogenic substrate. Thus, for example, one will desire to contact and incubate the second antibody-bound surface with a urease or peroxidase-conjugated anti-human IgG for a period of time and under conditions which favor the development of immunocomplex formation (*e.g.*, incubation for 2 hr at room temperature in a PBS-containing solution such as PBS/Tween®).

After incubation with the second enzyme-tagged antibody, and subsequent to washing to remove unbound material, the amount of label is quantified by incubation with a chromogenic substrate such as urea and bromocresol purple or 2,2'-azino-di-(3-ethyl-benzthiazoline)-6-sulfonic acid (ABTS) and H_2O_2, in the case of peroxidase as the enzyme label. Quantitation is then achieved by measuring the degree of color generation, *e.g.*, using a visible spectrum spectrophotometer.

The preceding format may be altered by first binding the sample to the assay plate. Then, primary antibody is incubated with the assay plate, followed by detecting of

bound primary antibody using a labeled second antibody with specificity for the primary antibody.

The antibody compositions of the present invention will find great use in immunoblot or Western blot analysis. The antibodies may be used as high-affinity primary reagents for the identification of proteins immobilized onto a solid support matrix, such as nitrocellulose, nylon or combinations thereof. In conjunction with immunoprecipitation, followed by gel electrophoresis, these may be used as a single step reagent for use in detecting antigens against which secondary reagents used in the detection of the antigen cause an adverse background. Immunologically-based detection methods for use in conjunction with Western blotting include enzymatically-, radiolabel-, or fluorescently-tagged secondary antibodies against the toxin moiety are considered to be of particular use in this regard.

V. Cardiomyocyte Regeneration

The present invention also involves, in another embodiment, the treatment of the loss of cardiomycoytes, for example due to myocardial infarction. In particular, myocardin plays a role in cardiac myocyte development. Thus, increasing levels of myocardin in non-cardiomyocyte target cells can be used to modulate the phenotype of such target cells such that it includes one or more functions of cardiomyocytes, whereas decreasing the levels of myocardin activity in cardiomyocytes can be used to reduce or inhibit one or more cardiomyocyte functionalities and promote cell growth.

One of the therapeutic embodiments contemplated by the present inventors is the intervention, at the molecular level, in the events involved in cardiomyocyte development. Specifically, the present inventors intend to provide, to a non-cardiomyocyte target cell, for example a cardiac fibroblast cell, an expression construct capable of providing myocardin to that cell. The lengthy discussions of gene delivery means, expression vectors and the genetic elements employed therein are incorporated into this section by reference. Exemplary gene delivery vectors are viral vectors such as adenovirus, adeno-associated virus, herpesvirus, vaccinia virus, lentivirus and retrovirus, as well as lipid-based vectors.

A. Gene Therapy

One skilled in the art recognizes that various methods of DNA delivery may be employed to deliver the polynucleotides of the present invention to specific cells for gene therapy. Further, in the context of gene therapy, a skilled artisan is cognizant that the vector to be utilized will generally contain the gene of interest operatively linked to a promoter. One skilled in the art also recognizes that, in certain instances, other sequences such as a 5' and/or 3'-UTR regulatory sequences are useful in expressing the gene of interest.

Where appropriate, the gene therapy vectors can be formulated into preparations in solid, semisolid, liquid or gaseous forms in the ways known in the art for their respective route of administration. Means known in the art can be utilized to prevent release and absorption of the composition until it reaches the target organ or to ensure timed release of the composition. Alternatively or additionally, the composition may be targeted by the delivery itself, for example by intracoronary delivery to target the heart (see *e.g.* U.S. Patents 5,792,453 and 6,100,242, hereby incorporated by reference in their entirety). A pharmaceutically acceptable form should be employed which does not deactivate the compositions of the present invention. In pharmaceutical dosage forms, the compositions can be used alone or in appropriate association, as well as in combination, with other pharmaceutically active compounds. Preferably, a sufficient amount of vector containing the therapeutice nucleic acid sequence is administered to provide a pharmacologically effective dose of the gene product, for example to alleviate symptoms associated with the disease being treated.

One skilled in the art recognizes that other methods of delivery may likewise be utilized to administer an expression cassette into a cell. Examples include: (1) methods utilizing physical means, such as electroporation (electricity), a gene gun (physical force) or applying large volumes of a liquid (pressure); and (2) methods wherein said expression cassette is complexed with another entity, such as a lipid-based vector (*e.g.*, a liposome), an aggregated protein or a transporter molecule. Certain of these embodiments are primarily suitable for *ex vivo* applications.

The actual dose and schedule can vary, for example, depending on whether the compositions are administered in combination with other pharmaceutical compositions, or depending on inter-individual differences in pharmacokinetics, drug disposition, and metabolism. Similarly, amounts to be administered can vary in *in vitro* applications, for example depending on the particular cell line utilized (*e.g.,* based on the variable number and/or type of vector receptors present on the cell surface, or the ability of the particular vector employed for gene transfer to replicate in that cell line). Furthermore, the amount of vector to be added per cell will likely vary with the length and stability of the therapeutic gene inserted in the vector, as well as the nature of the sequence itself. Thus, vector amount is particularly a parameter which is preferably determined empirically and can be altered due to factors not inherent to the present invention (for instance, the cost associated with synthesis). One skilled in the art can easily make adjustments to dose in accordance with the exigencies of the particular situation.

Those of skill in the art are well aware of how to apply gene delivery to *in vivo* situations. By way of illustration, for viral vectors, one generally will prepare a viral vector stock. Depending on the type of virus utilized and the titer attainable, one will generally deliver 1 X 10^4, 1 X 10^5, 1 X 10^6, 1 X 10^7, 1 X 10^8, 1 X 10^9, 1 X 10^{10}, 1 X 10^{11}, 1 X 10^{12} to 10^{13} infectious particles to the patient. Similar figures may be extrapolated for lipid-based or other non-viral formulations by comparing relative uptake efficiencies. Formulation as a pharmaceutically acceptable composition is discussed further below. Various routes are contemplated, but local provision to the heart, preferably by the method of Hammond, et al., *supra* and intra-arterial or intravenous administration are preferred.

In another embodiment, it is contemplated that blocking myocardin activity may result in stimulation of the cardiomycytes to divide. This may be accomplished in one of several ways. First, one may provide an analog of myocardin's target that binds and inhibits myocardin function, effectively creating a "suicide substrate" for myocardin. This approach also could be exploited using a mimetic (see above). Second, one could use a similar peptide target, with an additional domain actually capable of cleaving myocardin. Third, one could provide a non-functional myocardin analog that is capable

of competing with myocardin peptide. And fourth, antisense or ribozyme techniques could also be used to inhibit the expression of myocardin.

B. Combined Therapy

In another embodiment, it is envisioned to use myocardin in combination with other therapeutic modalities. For example, it is known that myocardin interacts with other transcription factors. Thus, the present invention further contemplates the provision of myocardin in conjunction with one or more transcription factors, and in particular, one or more cardiac transcription factors. Examples of cardiac transcription factors include, but are not limited to, GATA4, serum response factor (SRF) and Nkx2.5.

In other embodiments, in addition to the therapies described above, one may also provide to the patient more "standard" pharmaceutical cardiac therapies. Examples of standard therapies include, without limitation, so-called "beta blockers", anti-hypertensives, cardiotonics, anti-thrombotics, vasodilators, hormone antagonists, endothelin antagonists, calcium channel blockers, phosphodiesterase inhibitors, angiotensin type 2 antagonists and cytokine blockers/inhibitors.

Combinations may be achieved by contacting cardiac cells with a single composition or pharmacological formulation that includes both agents, or by contacting the cell with two distinct compositions or formulations, at the same time, wherein one composition includes the expression construct and the other includes the agent. Alternatively, gene therapy may precede or follow administration of the other agent by intervals ranging from minutes to weeks. In embodiments where the other agent and expression construct are applied separately to the cell, one would generally ensure that a significant period of time did not expire between the time of each delivery, such that the agent and expression construct would still be able to exert an advantageously combined effect on the cell. In such instances, it is contemplated that one would typically contact the cell with both modalities within about 12-24 hours of each other and, more preferably, within about 6-12 hours of each other, with a delay time of only about 12 hours being most preferred. In some situations, it may be desirable to extend the time

period for treatment significantly, however, where several days (2, 3, 4, 5, 6 or 7) to several weeks (1, 2, 3, 4, 5, 6, 7 or 8) lapse between the respective administrations.

It also is conceivable that more than one administration of either a myocardin gene, or the other agent will be desired. In this regard, various combinations may be employed. By way of illustration, where myocardin is "A" and the other agent or cardiac transcription factor is "B," the following permutations based on 3 and 4 total administrations are exemplary:

A/B/A B/A/B B/B/A A/A/B B/A/A A/B/B B/B/B/A B/B/A/B

A/A/B/B A/B/A/B A/B/B/A B/B/A/A B/A/B/A B/A/A/B B/B/B/A

A/A/A/B B/A/A/A A/B/A/A A/A/B/A A/B/B/B B/A/B/B B/B/A/B

Other combinations are likewise contemplated.

VII. Drug Formulations and Routes for Administration to Patients

Where clinical applications are contemplated, pharmaceutical compositions will be prepared – *e.g.*, expression vectors, virus stocks and drugs - in a form appropriate for the intended application. Generally, this will entail preparing compositions that are essentially free of pyrogens, as well as other impurities that could be harmful to humans or animals.

One will generally desire to employ appropriate salts and buffers to render delivery vectors stable and allow for uptake by target cells. Buffers also will be employed when recombinant cells are introduced into a patient. Aqueous compositions of the present invention comprise an effective amount of the vector or cells, dissolved or dispersed in a pharmaceutically acceptable carrier or aqueous medium. The phrase "pharmaceutically or pharmacologically acceptable" refer to molecular entities and compositions that do not produce adverse, allergic, or other untoward reactions when administered to an animal or a human. As used herein, "pharmaceutically acceptable carrier" includes solvents, buffers, solutions, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents and the like acceptable for use

in formulating pharmaceuticals, such as pharmaceuticals suitable for administration to humans. The use of such media and agents for pharmaceutically active substances is well know in the art. Except insofar as any conventional media or agent is incompatible with the active ingredients of the present invention, its use in therapeutic compositions is contemplated. Supplementary active ingredients also can be incorporated into the compositions, provided they do not inactivate the vectors or cells of the compositions.

The active compositions of the present invention may include classic pharmaceutical preparations. Administration of these compositions according to the present invention may be via any common route so long as the target tissue is available via that route. This includes oral, nasal, buccal, rectal, vaginal or topical. Alternatively, administration may be by orthotopic, intradermal, subcutaneous, intramuscular, intraperitoneal or intravenous injection. Such compositions would normally be administered as pharmaceutically acceptable compositions, as described *supra*.

The active compounds may also be administered parenterally or intraperitoneally. By way of illustration, solutions of the active compounds as free base or pharmacologically acceptable salts can be prepared in water suitably mixed with a surfactant, such as hydroxypropylcellulose. Dispersions can also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof and in oils. Under ordinary conditions of storage and use, these preparations generally contain a preservative to prevent the growth of microorganisms.

The pharmaceutical forms suitable for injectable use include, for example, sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions. Generally, these preparations are sterile and fluid to the extent that easy syringability exists. Preparations should be stable under the conditions of manufacture and storage and should be preserved against the contaminating action of microorganisms, such as bacteria and fungi. Appropriate solvents or dispersion media may contain, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), suitable mixtures thereof, and vegetable oils. The proper fluidity can be maintained, for example, by the use of a

coating, such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. The prevention of the action of microorganisms can be brought about by various antibacterial an antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions may be prepared by incorporating the active compounds in an appropriate amount into a solvent along with any other ingredients (for example as enumerated above) as desired, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the various sterilized active ingredients into a sterile vehicle which contains the basic dispersion medium and the desired other ingredients, *e.g.*, as enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation include vacuum-drying and freeze-drying techniques which yield a powder of the active ingredient(s) plus any additional desired ingredient from a previously sterile-filtered solution thereof.

For oral administration the polypeptides of the present invention generally may be incorporated with excipients and used in the form of non-ingestible mouthwashes and dentifrices. A mouthwash may be prepared incorporating the active ingredient in the required amount in an appropriate solvent, such as a sodium borate solution (Dobell's Solution). Alternatively, the active ingredient may be incorporated into an antiseptic wash containing sodium borate, glycerin and potassium bicarbonate. The active ingredient may also be dispersed in dentifrices, including: gels, pastes, powders and slurries. The active ingredient may be added in a therapeutically effective amount to a paste dentifrice that may include water, binders, abrasives, flavoring agents, foaming agents, and humectants.

The compositions of the present invention generally may be formulated in a neutral or salt form. Pharmaceutically-acceptable salts include, for example, acid

addition salts (formed with the free amino groups of the protein) derived from inorganic acids (*e.g.*, hydrochloric or phosphoric acids, or from organic acids (*e.g.*, acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups of the protein can also be derived from inorganic bases (*e.g.*, sodium, potassium, ammonium, calcium, or ferric hydroxides) or from organic bases (*e.g.*, isopropylamine, trimethylamine, histidine, procaine and the like.

Upon formulation, solutions are preferably administered in a manner compatible with the dosage formulation and in such amount as is therapeutically effective. The formulations may easily be administered in a variety of dosage forms such as injectable solutions, drug release capsules and the like. For parenteral administration in an aqueous solution, for example, the solution generally is suitably buffered and the liquid diluent first rendered isotonic for example with sufficient saline or glucose. Such aqueous solutions may be used, for example, for intravenous, intramuscular, subcutaneous and intraperitoneal administration. Preferably, sterile aqueous media are employed as is known to those of skill in the art, particularly in light of the present disclosure. By way of illustration, a single dose may be dissolved in 1 ml of isotonic NaCl solution and either added to 1000 ml of hypodermoclysis fluid or injected at the proposed site of infusion, (see for example, "Remington's Pharmaceutical Sciences" 15th Edition, pages 1035-1038 and 1570-1580). Some variation in dosage will necessarily occur depending on the condition of the subject being treated. The person responsible for administration will, in any event, determine the appropriate dose for the individual subject. Moreover, for human administration, preparations should meet sterility, pyrogenicity, general safety and purity standards as required by FDA Office of Biologics standards.

VIII. Methods of Making Transgenic Mice

A particular embodiment of the present invention provides transgenic animals that contain myocardin-related constructs. Transgenic animals expressing myocardin, recombinant cell lines derived from such animals, and transgenic embryos may be useful in determining the exact role that myocardin plays in the development and differentiation of cardiomyocytes. Furthermore, this transgenic animal may provide an insight into heart development. The use of constitutively expressed myocardins provides a model for over-

or unregulated expression. Also, transgenic animals which are "knocked out" for myocardin, in one or both alleles are contemplated.

In a general aspect, a transgenic animal is produced by the integration of a given transgene into the genome in a manner that permits the expression of the transgene. Methods for producing transgenic animals are generally described by Wagner and Hoppe (U.S. Patent 4,873,191; which is incorporated herein by reference), Brinster *et al.,* 1985; which is incorporated herein by reference in its entirety) and in Hogan *et al.* (1994).

Typically, a gene flanked by genomic sequences is transferred by microinjection into a fertilized egg. The microinjected eggs are implanted into a host female, and the progeny are screened for the expression of the transgene. Transgenic animals may be produced from the fertilized eggs from a number of animals including, but not limited to reptiles, amphibians, birds, mammals, and fish.

DNA clones for microinjection can be prepared by any means known in the art. For example, DNA clones for microinjection can be cleaved with enzymes appropriate for removing the bacterial plasmid sequences, and the DNA fragments electrophoresed on 1% agarose gels in TBE buffer, using standard techniques. The DNA bands are visualized by staining with ethidium bromide, and the band containing the expression sequences is excised. The excised band is then placed in dialysis bags containing 0.3 M sodium acetate, pH 7.0. DNA is electroeluted into the dialysis bags, extracted with a 1:1 phenol:chloroform solution and precipitated by two volumes of ethanol. The DNA is redissolved in 1 ml of low salt buffer (0.2 M NaCl, 20 mM Tris,pH 7.4, and 1 mM EDTA) and purified on an Elutip-D™ column. The column is first primed with 3 ml of high salt buffer (1 M NaCl, 20 mM Tris, pH 7.4, and 1 mM EDTA) followed by washing with 5 ml of low salt buffer. The DNA solutions are passed through the column three times to bind DNA to the column matrix. After one wash with 3 ml of low salt buffer, the DNA is eluted with 0.4 ml high salt buffer and precipitated by two volumes of ethanol. DNA concentrations are measured by absorption at 260 nm in a UV spectrophotometer. For microinjection, DNA concentrations are adjusted to 3 μg/ml in 5 mM Tris, pH 7.4 and 0.1 mM EDTA. Other methods for purification of DNA for

microinjection are described in Hogan *et al.* (1986), in Palmiter *et al.* (1982); and in Sambrook *et al.* (1989).

In an exemplary microinjection procedure, female mice six weeks of age are induced to superovulate with a 5 IU injection (0.1 cc, ip) of pregnant mare serum gonadotropin (PMSG; Sigma) followed 48 hours later by a 5 IU injection (0.1 cc, ip) of human chorionic gonadotropin (hCG; Sigma). Females are placed with males immediately after hCG injection. Twenty-one hours after hCG injection, the mated females are sacrificed by $C0_2$ asphyxiation or cervical dislocation and embryos are recovered from excised oviducts and placed in Dulbecco's phosphate buffered saline with 0.5% bovine serum albumin (BSA; Sigma). Surrounding cumulus cells are removed with hyaluronidase (1 mg/ml). Pronuclear embryos are then washed and placed in Earle's balanced salt solution containing 0.5 % BSA (EBSS) in a 37.5°C incubator with a humidified atmosphere at 5% CO_2, 95% air until the time of injection. Embryos can be implanted at the two-cell stage.

Randomly cycling adult female mice are paired with vasectomized males. C57BL/6 or Swiss mice or other comparable strains can be used for this purpose. Recipient females are mated at the same time as donor females. At the time of embryo transfer, the recipient females are anesthetized with an intraperitoneal injection of 0.015 ml of 2.5 % avertin per gram of body weight. The oviducts are exposed by a single midline dorsal incision. An incision is then made through the body wall directly over the oviduct. The ovarian bursa is then torn with watchmakers forceps. Embryos to be transferred are placed in DPBS (Dulbecco's phosphate buffered saline) and in the tip of a transfer pipet (about 10 to 12 embryos). The pipet tip is inserted into the infundibulum and the embryos transferred. After the transfer, the incision is closed by two sutures.

IX. Screening Assays

The present invention also contemplates the screening of compounds for various abilities to interact with and/or affect myocardin expression or function. Particularly preferred compounds will be those useful in inhibiting or promoting the actions of myocardin in regulating the development and differentiation of cardiomyocytes. In the screening assays of the present invention, the candidate substance may first be screened for basic biochemical activity -- *e.g.,* binding to a target molecule -- and then tested for its ability to inhibit modulate activity, at the cellular, tissue or whole animal level.

A. Modulators and Assay Formats

i) Assay Formats

The present invention provides methods of screening for modulators of myocardin expression and binding to other proteins or nucleic acids. In one embodiment, the present invention is directed to a method of:

(a) providing a myocardin polypeptide;

(b) contacting the myocardin polypeptide with the candidate substance; and

(c) determining the binding of the candidate substance to myocardin polypeptide.

In yet another embodiment, the assay looks not at binding, but at myocardin function. Such methods would comprise, for example:

(a) providing myocardin and GATA to a cell;

(b) admixing myocardin and GATA in the presence of a candidate modulator; and

(c) measuring the effect of the candidate substance on the expression of a cardiac cell gene product.

A related assay that examines the interaction of myocardin and GATA would comprise:

(a) providing myocardin and GATA to a cell;

(b) admixing myocardin and GATA in the presence of a candidate substance; and

(c) measuring the effect of the candidate substance on the interaction of myocardin and GATA.

Both of the preceding assays could be performed substituting SRF or Nkx2.5 for GATA.

In still yet other embodiments, one would look at the effect of a candidate substance on the expression of myocardin. This can be done by examining mRNA expression, although alterations in mRNA stability and translation would not be accounted for. A more direct way of assessing expression is by directly examining protein levels, for example, through Western blot or ELISA.

ii) Inhibitors and Activators

An inhibitor according to the present invention may be one which exerts an inhibitory effect on the expression or function of myocardin. By the same token, an activator according to the present invention may be one which exerts a stimulatory effect on the expression or function of myocardin.

iii) Candidate Substances

As used herein, the term "candidate substance" refers to any molecule that may potentially modulate myocardin expression or function. The candidate substance may be a protein or fragment thereof, a small molecule inhibitor, or even a nucleic acid molecule. It may prove to be the case that the most useful pharmacological compounds will be compounds that are structurally related to compounds which interact naturally with myocardin. Creating and examining the action of such molecules is known as "rational drug design," and include making predictions relating to the structure of target molecules.

The goal of rational drug design is to produce structural analogs of biologically active polypeptides or target compounds. By creating such analogs, it is possible to fashion drugs which are more active or stable than the natural molecules, which have different susceptibility to alteration or which may affect the function of various other molecules. In one approach, one would generate a three-dimensional structure for a molecule like myocardin, and then design a molecule for its ability to interact with myocardin. Alternatively, one could design a partially functional fragment of myocardin (binding, but no activity), thereby creating a competitive inhibitor. This could be accomplished by x-ray crystallography, computer modeling or by a combination of both approaches.

It also is possible to use antibodies to ascertain the structure of a target compound or inhibitor. In principle, this approach yields a pharmacore upon which subsequent drug design can be based. It is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of anti-idiotype would be expected to be an analog of the original antigen. The anti-idiotype could then be used to identify and isolate peptides from banks of chemically- or biologically-produced peptides. Selected peptides would then serve as the pharmacore. Anti-idiotypes may be generated using the methods described herein for producing antibodies, using an antibody as the antigen.

On the other hand, one may simply acquire, from various commercial sources, small molecule libraries that are believed to meet the basic criteria for useful drugs in an effort to "brute force" the identification of useful compounds. Screening of such libraries, including combinatorially generated libraries (*e.g.*, peptide libraries), is a rapid and efficient way to screen large number of related (and unrelated) compounds for activity. Combinatorial approaches also lend themselves to rapid evolution of potential drugs by the creation of second, third and fourth generation compounds modeled of active, but otherwise undesirable compounds.

Candidate compounds may include fragments or parts of naturally-occurring compounds or may be found as active combinations of known compounds which are otherwise inactive. It is proposed that compounds isolated from natural sources, such as animals, bacteria, fungi, plant sources, including leaves and bark, and marine samples may be assayed as candidates for the presence of potentially useful pharmaceutical agents. It will be understood that the pharmaceutical agents to be screened could also be derived or synthesized from chemical compositions or man-made compounds. Thus, it is understood that the candidate substance identified by the present invention may be polypeptide, polynucleotide, small molecule inhibitors or any other compounds that may be designed through rational drug design starting from known inhibitors of hypertrophic response.

Other suitable inhibitors include antisense molecules, ribozymes, and antibodies (including single chain antibodies).

It will, of course, be understood that the screening methods of the present invention are useful in themselves notwithstanding the fact that effective candidates may not be found. The invention provides methods for screening for such candidates, not solely methods of finding them.

B. *In Vitro* Assays

A quick, inexpensive and easy assay to run is a binding assay. Binding of a molecule to a target may, in and of itself, be inhibitory, due to steric, allosteric or charge-charge interactions. This can be performed in solution or on a solid phase and can be

utilized as a first round screen to rapidly eliminate certain compounds before moving into more sophisticated screening assays. In one embodiment of this kind, the screening of compounds that bind to a myocardin molecule or fragment thereof is provided

The target may be either free in solution, fixed to a support, expressed in or on the surface of a cell. Either the target or the compound may be labeled, thereby permitting determining of binding. In another embodiment, the assay may measure the inhibition of binding of a target to a natural or artificial substrate or binding partner (such as myocardin). Competitive binding assays can be performed in which one of the agents (myocardin for example) is labeled. Usually, the target will be the labeled species, decreasing the chance that the labeling will interfere with the binding moiety's function. One may measure the amount of free label versus bound label to determine binding or inhibition of binding.

A technique for high throughput screening of compounds is described in WO 84/03564. Large numbers of small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. The peptide test compounds are reacted with, for example, myocardin and washed. Bound polypeptide is detected by various methods.

Purified target, such as myocardin, can be coated directly onto plates for use in the aforementioned drug screening techniques. However, non-neutralizing antibodies to the polypeptide can be used to immobilize the polypeptide to a solid phase. Also, fusion proteins containing a reactive region (preferably a terminal region) may be used to link an active region (*e.g.,* the C-terminus of myocardin) to a solid phase.

C. *In Cyto* Assays

Various cell lines that express myocardin can be utilized for screening of candidate substances. For example, cells containing myocardin with an engineered indicators can be used to study various functional attributes of candidate compounds. In such assays, the compound would be formulated appropriately, given its biochemical nature, and contacted with a target cell.

Depending on the assay, culture may be required. As discussed above, the cell may then be examined by virtue of a number of different physiologic assays (growth, size, Ca^{++} effects). Alternatively, molecular analysis may be performed in which the function of myocardin and related pathways may be explored. This involves assays such as those for protein expression, enzyme function, substrate utilization, mRNA expression (including differential display of whole cell or polyA RNA) and others.

D. *In Vivo* Assays

The present invention particularly contemplates the use of various animal models. Transgenic animals may be created with constructs that permit myocardin expression and activity to be controlled and monitored. The generation of these animals has been described elsewhere in this document.

Treatment of these animals with test compounds will involve the administration of the compound, in an appropriate form, to the animal. Administration will be by any route the could be utilized for clinical or non-clinical purposes, including but not limited to oral, nasal, buccal, or even topical. Alternatively, administration may be by intratracheal instillation, bronchial instillation, intradermal, subcutaneous, intramuscular, intraperitoneal or intravenous injection. Specifically contemplated are systemic intravenous injection, regional administration via blood or lymph supply.

E. Production of Inhibitors

In an extension of any of the previously described screening assays, the present invention also provide for methods of producing inhibitors. The methods comprising any of the preceding screening steps followed by an additional step of "producing the candidate substance identified as a modulator of" the screened activity.

X. Examples

The following examples are included to further illustrate various aspects of the invention. It should be appreciated by those of skill in the art that the techniques disclosed in the examples which follow represent techniques and/or compositions discovered by the inventor to function well in the practice of the invention, and thus can

be considered to constitute preferred modes for its practice. However, those of skill in the art should, in light of the present disclosure, appreciate that many changes can be made in the specific embodiments which are disclosed and still obtain a like or similar result without departing from the spirit and scope of the invention.

EXAMPLE 1

Expression Pattern of Myocardin 1 During Early Heart Development

The heart is the first organ to form during mammalian development. Cardiac muscle cells originate from a region of the embryo known as the cardiac crescent and develop into a primitive heart tube along the midline of the embryo (FIG. 1). Because this is the only region of the embryo that can give rise to cardiac muscle cells, it would be expected to express a unique set of genes responsible for cardiogenesis. By identifying the genes that are uniquely expressed in this region, master control genes for heart formation can be identified. Subsequent embryonic events of looping, chamber maturation and alignment with the vascular system give rise to the mature four-chambered heart (Olson *et al.*, 1996 and Fishman *et al.,* 1997).

Expression of myocardin 1 was determined by whole-mount (FIG. 3A) or section (FIG. 3B and FIG. 3C) *in situ* hybridizations to mouse embryos at E7.75 (FIG. 3A), E8.0 (FIG. 3B), and E12.5 (FIG. 3C).

In situ hybridization to cellular RNA was performed using standard techniques well known in the art, *e.g.,* fluorescence *in situ* hybridization (FISH). Briefly, the samples were fixed for the appropriate time and dehydrated through a graded ethanol series. The samples were then impregnated in paraffin wax and cast into blocks. The samples were sectioned on a microtome. A specific labeled probe was prepared. The probe can be labeled with biotin or digoxigenin or with a fluorochrome-tagged deoxynucleotide. Next, the probe was hybrized to the sample. Hybridization conditions may vary with the different labeled probes. After the hybridization, samples were washed for 15 min in 37°C 50% formamide/2 × SSC, 15 min in 37°C 2 × SSC and 15 min in room temperature 1 × SSC. The slides were equilibrated for 5 min in 4 × SSC at room temperature. The slides were drained and allowed to air dray. Next, a detection

solution was added. After a 45 min incubation in the detection solution, the slides were washed. A counterstain of DAPI or propidium iodide staining solution was added to the slide. The slide was viewed using a fluorescence microscope.

The results in FIG. 3 illustrate the expression pattern of myocardin 1 during early heart development. In FIG. 3A, myocardin 1 transcripts can be seen localized to the cardiac crescent. In FIG. 3B, transcripts are present throughout the heart tube in a transverse section. In FIG. 3C, transcripts are seen throughout the developing heart in a sagittal section.

As might be expected given its role in embryonic development, myocardin has also been shown to be expressed in a subset of embryonic vascular and visceral smooth muscle cells. At E13.5, myocardin expression was evident within smooth muscle cells lining the walls of the esophagus and aortic arch arteries, as well as the pulmonary outflow tract. Expression in these smooth muscle cell types was still apparent, but was diminished, by E15.5. Myocardin expression was also detected in smooth muscle cells within the lung and gut, as well as in head mesenchyme, which may serve as a source of smooth muscle precursors. Myocardin was not expressed at detectable levels in skeletal muscle.

EXAMPLE 2

Expression Pattern of Myocardin 1 in Adult Mouse Tissues

The expression of myocardin 1 transcripts in adult mouse tissues was analyzed by Northern blot, utilizing techniques well known in the art. RNA was isolated from adult mouse heart, brain, spleen, lung, liver, skeletal muscle, kidney and testis according to standard RNA isolation procedures, *e.g.,* phenol/chloroform/isoamyl alcohol (RNAzol, Life Technologies, Inc.) or guanidine thiocyanate.

Briefly, fractionated RNA was transferred from an agarose gel to a membrane by upward capillary action. The transferred RNA is cross-linked to the membrane. Next, a radiolabeled probe (DNA or RNA) was hybridized to the membrane in a formamide solution. After hybridization, autoradiography was performed to detect the transcripts.

The results in FIG. 4 show that the transcripts were detected only in the heart. A RNA molecular marker illustrates the size of the transcripts.

EXAMPLE 3

Nuclear Localization of Myocardin 1 Protein

Cos cells were transiently transfected with an expression vector encoding myocardin 1 with a Flag-epitope tag. Transient transfection assays were performed using standard methods, such as LifofectAMINE plus (Life Technologies, Inc.), calcium phosphate or electroporation. Briefly, the cells were plated 12 hr before transfection in tissue culture dishes. They were transfected with a total of about 0.5–1.0 μg of plasmid DNA. The subcellular location of myocardin 1 protein was determined by immunostaining with anti-Flag antibody.

All myocardin 1 protein is localized to the nucleus as illustrated in FIG. 5. The inset in the lower right corner shows an enlargement of a single cell, with strong myocardin 1 staining in the nucleus, but excluded from the nucleoli.

EXAMPLE 4

Structure of Myocardin 1 and Mapping of Transcription Activation Domains

Portions of myocardin 1 were fused to the DNA binding domain of yeast GAL4 and tested in transfected Cos cells for transcriptional activity against a GAL4-dependent luciferase reporter. The relative transcriptional activities of different myocardin 1 fragments are show in FIG. 6.

The nuclear localization sequence (NLS) is located between residues 245 and 254, within a basic region at residues 243-260. A glutamine-rich (Q) domain is located between residues 287-320. The SAP domain is found at residues 380-414. The transcription activation domain is located at the carboxyl-terminus at 670 to 935. The carboxyl-terminus is an extremely potent transcription activation domain, able to activate the reporter over 1000-fold, to a level comparable to that of the powerful viral coactivator VP16 (not shown).

As might be expected, given its apparent influence on transcription, myocardin contains an SAP domain (named for nuclear scaffold attachment factors A and B), as found in a variety of proteins that affect not only transcription but also nuclear architecture. The SAP domain is a 35 amino acid motif containing two predicted amphipathic helices separated by an intervening region with an invariant glycine residue. Functional aspects of the SAP domain were examined by introducing proline mutations into helix-1 or –2. These mutations had only a modest effect on the ability of myocardin to transactivate the *SM22* promoter (which transactivtation is discussed further below). Similarly, the deletion of the linker region between the two helices of the SAP domain, shown previously to be required for DNA binding by SAF-A, had little effect on *SM22* activation, but eliminated *ANF* activation (discussed below).

EXAMPLE 5

Trans-Activation of the SM22 Promoter by Myocardin

Cos cells were transiently transfected with a luciferase reporter gene containing the 1.4 kb *SM22* promoter and expression vectors encoding myocardin 1 and SRF. Briefly, the cells were plated 12 hr before transfection in tissue culture dishes. They were transfected with plasmid DNA. Forty eight hr after transfection, the cells were harvested. Luciferase assays of whole cell extracts were conducted by standard methods well known in the art.

FIG. 7A shows activity of the wild-type *SM22* promoter, which was transactivated about 100-fold by myocardin. FIG. 7B shows activity of the *SM22* promoter with a mutation in the distal CArG box (CArG-far). This promoter was also activated by myocardin, but not to the same extent as the wild-type promoter. FIG. 7C shows activity of the *SM22* promoter with a mutation in the proximal CArG box (CArG-near). This promoter has lost almost all responsiveness to myocardin, as has the promoter with both the CArG boxes mutated (FIG. 7D). Both myocardin 1 and N-terminally truncated myocardin 1 have demonstrated similar activities in these assays.

Additional studies have further demonstrated myocardin's potency as a transactivator and its preferential action via CArG boxes. By way of example,

myocardin's ability to transactivate reporter genes containing four tandem copies of *SM22* CArG-near or the c-*fos* SRE linked to the E1b promoter was tested and compared to SRF. These reporters were transactivated several hundred-fold by myocardin, whereas SRF was only able to activate expression by 8-fold.

EXAMPLE 6

Myocardin 1 and MEF2C Cooperatively Activate the MLC2V Promoter

Cos cells were transiently transfected with a luciferase reporter gene containing the MLC2V promoter and expression vectors encoding myocardin 1 and MEF2C, as indicated. Forty eight hr later, cells were harvested and luciferase activity was assayed. The results in FIG. 8 show that myocardin 1 and MEF2C synergistically activate MLC2V transcription. Both myocardin 1 and N-terminally truncated myocardin 1 have demonstrated similar activities in these assays.

EXAMPLE 7

Interactions of Myocardin 1 and GATA4

A. GATA4 Represses Myocardin Activation of the ANF Promoter

HeLa cells and Cos cells were transiently transfected with a luciferase reporter gene containing the ANF promoter and expression vectors encoding myocardin 1 and GATA4, as indicated. Forty eight hr later, cells were harvested and luciferase activity was assayed. The results in FIG. 9 show that GATA4 represses myocardin 1 activation of ANF transcription.

B. Myocardin 1 and GATA4 Cooperatively Activate the Nkx2.5 Promoter

HeLa cells (and/or Cos cells) were transiently transfected with a luciferase reporter gene containing the Nkx2.5 promoter and expression vectors encoding myocardin 1 and GATA4. Approximately forty eight hr later, cells were harvested and luciferase activity was assayed. The results demonstrated that myocardin 1 and GATA4 cooperatively activated Nkx2.5 transcription. Both myocardin 1 and N-terminally

truncated myocardin 1 have demonstrated similar activities in these GATA4 interaction assays. FIG. 13.

EXAMPLE 8

Myocardin 1 and Nkx2.5 Cooperatively Activate the α-MHC Promoter

HeLa cells were transiently transfected with a luciferase reporter gene containing the α-MHC promoter and expression vectors encoding myocardin 1 and Nkx2.5. Forty eight hr later, cells were harvested and luciferase activity was assayed. The results in FIG. 10 show that myocardin 1 and Nkx2.5 synergistically activate α-MHC transcription. **EXAMPLE 9Myocardin Forms a Complex with SRF**To further examine the mechanism for CArG box-dependent transcriptional activation, the inventors tested whether myocardin translated *in vitro* could bind to the CArG boxes from the *SM22* promoter. SRF bound to both CArG boxes, but no binding of myocardin to either CArG box was detectable in gel mobility shift assays. However, myocardin in the presence of SRF gave rise to a prominent ternary complex with the CArG box sequence. This ternary complex was supershifted by antibodies against SRF or FLAG-tagged myocardin. The total amount of SRF DNA binding was comparable in the presence and absence of myocardin, suggesting that association of SRF with myocardin does not alter the affinity of SRF fro the CArG box. Myocardin and SRF also formed a ternary complex with the c-*fos* and *ANF* CArG boxes, the intensity of which correlated directly with the relative binding of SRF to the site. The lack of obvious homology in the flanking sequences of these different CArG boxes suggests that myocardin associates directly with SRF and does not depend on specific DNA sequences for ternary complex formation.

The region of myocardin required for ternary complex formation with SRF was determined using myocardin deletion mutants. Deletion of the amino-terminal 276 amino acid abolished association with SRF, as did larger amino-terminal deletions. In contrast, deletions from near the middle of the protein to the carboxyl terminus did not affect SRF interaction. Deletion of the Q-rich domain or the basic regions also abolished ternary complex formation, whereas mutation of the SAP domain did not. These findings are consistent with the interpretation that the amino terminus of myocardin confers

transcriptional specificity by mediating association with SRF, whereas the carboxyl terminus activates transcription.

To determine whether myocardin interacts with the DNA binding or transcription activation domain of SRF, the inventors performed gel mobility shift assays with an SRF deletion mutant encompassing the MADS domain, but lacking the amino and carboxyl termini. This SRF mutation (SRF 100-300) bound the CArG box sequence and formed a ternary complex with myocardin.

Association of myocardin and SRF was also readily detectable in coimmunoprecipitation assays of epitope-tagged proteins. Interaction was dependent on the amino-terminal regions of myocardin. The core MADS domain of SRF (residues 133-266) was also necessary and sufficient to mediate association with myocardin in coimmunoprecipitation assays.

Without wishing to be bound by any particular theory, these results suggest that myocardin interacts with SRF to form a stable ternary complex which may be an aspect of the mechanism of action of myocardin as a transcription activator. Both myocardin 1 and N-terminally truncated myocardin 1 have demonstrated similar activities in this regard.

Myocardin has also been shown to be sensitive to the level of SRF, such that at low concentrations of SRF expression plasmid, myocardin and SRF synergistically activated *SM22* transcription, whereas at higher concentrations of SRF, transcriptional activation by myocardin was reduced. Inhibition of myocardin-dependent transcription by excess SRF could be relieved by increasing the amount of myocardin. Thus, the ratio of SRF to myocardin appears relevant for transcriptional activation by myocardin, such that exceeding an optimal ratio with an excess of SRF can result in attenuation of myocardin activity.

EXAMPLE 10

Inhibition of Cardiomyocyte Differentiation in *Xenopus* Embryos by Dominant Negative Myocardin

Further confirming the role of myocardin in cardiomyocyte differentiation, mRNA from a dominant negative myocardin mutant was injected into *Xenopus* embryos. A dramatic reduction in the expression of transcripts for cardiac α-actin and α-tropomyosin was observed. The effects on cardiac differentiation were highly specific as demonstrated by the normal overall appearance of the embryo. Also observed was a dose-dependent reduction in expression of cardiac markers, such that approximately 90% of injected embryos exhibited a reduction or complete elimination of cardiac gene expression.

EXAMPLE 11

Overexpression of Myocardin Induces Hypertrophy in Cardiomyocytes

The inventors have investigated how myocardin affects the growth and/or differentiation of cardiomyocytes by overexpressing myocardin in cardiomyocytes using adenoviral delivering system. Cardiomyocyte cultures were prepared by dissociation of 1-day-old neonatal rat hearts and were plated differentially to remove fibroblasts. Cells were plated on glass coverslips coated with 4 $\mu g/cm^2$ laminin in 4:1 Dulbecco's modified Eagle's medium (DMEM):199 medium with 10% horse serum and 5% fetal calf serum at a density of 5×10^4 cells/cm^2. Eighteen hours after plating, cells were changed into serum-free media and infected with adenoviruses expressing either myocardin or ß-galactosidase (as a control) at a multiplicity of infection (m.o.i.) of 100.

For immunofluorescence, cells were fixed in 3.7% formaldehyde on ice for 30 min, permeabilized with 0.1% Triton X-100 in phosphate-buffered saline (PBS) and blocked with 5% serum in PBS for 1 hour at room temperature. Cells were incubated with monoclonal anti-α-actinin (sarcomeric) or anti-ANF (atrial natriuretic factor) antibodies at a dilution of 1:200 in blocking buffer for 1 hour at 37°C, washed and incubated with fluorescein-conjugated horse anti-mouse IgG antibody at a dilution of 1:200 in blocking

buffer for 1 hour at 37°C. Following secondary antibody incubation, cells were washed with PBS.

The results are shown in FIGS. 11 and 12. Overexpression of myocardin in neonatal cardiomyocytes induces assembly of sacomeres and expression of atrium natriuretic factor (ANF), markers of cardiac hypertrophy.

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The following references, to the extent that they provide exemplary procedural or other details supplementary to those set forth herein, are specifically incorporated herein by reference.

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